

OM protein - protein search, using sw model

Run on: November 17, 2005, 08:49:56 ; Search time 39 Seconds
 (without alignments)
 249.177 Million cell updates/sec

Title: US-10-678-588A-8
 Perfect score: 459
 Sequence: 1 RBDQYRPLIANSRIMKKAL.....FEDYIEBLKVYKXYREXEG 101

Scoring table: BLOSSUM62
 Gapcp 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
 Listing first 45 summaries

Database : PIR_79,*
 1: pir1,*
 2: pir2,*
 3: pir3,*
 4: pir4,*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match length	DB ID	Description	
1	417.5	91.0	179	S22820	transcription factor NF-Y, CCAAT-binding, chain B - maize
2	407.5	88.8	228	T45874	N;Alternate names: CAAT-box DNA-binding protein C;Species: Zea mays (maize) C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004 C;Accession: S22820 R;Li, X.Y.; Mantovani, R.; van Huijsduijnen, R.H.; Andre, I.; Benoist, C.; Mathis, A.;Title: Evolutionary variation of the CCAAT-binding transcription factor NF-Y. A;Reference number: S22816; MUID:92195809; PMID:1549471
3	400.5	88.3	138	E84810	A;Residues: 1-179 <LIX> A;Cross-references: UNIPROT:P25209; EMBL:X59714 C;Superfamily: transcription factor HAP3 C;Keywords: DNA binding; transcription regulation P;30-119/Domain: DNA binding #status predicted <DNA>
4	400.5	87.3	161	G71407	Query Match 91.0%; Score 417.5; DB 2; Length 179; Best Local Similarity 83.2%; Pred. No. 3.2e-47; 8; Matches 84; Conservative 2; Mismatches 7; Indels 7; Gaps 1;
5	393.5	85.7	178	A84788	Db 30 REQDELPIANSRIMKKALPANGK-----IADAKETVQECYSEFISPFITSERASDK 82
6	376.5	82.0	215	F84508	QY 61 QXERKRTTINGDDLLWAMATIGFEDYIEPLKVYKXYREXEG 101
7	375.5	73.5	180	S22489	Db 83 QRERKRTTINGDDLLWAMATIGFEDYIEPLKVYQKREMEG 123
8	337.5	73.5	205	F38245	RESULT 2
9	337.5	73.5	207	A23692	T45874 transcription factor NF-Y, CCAAT-binding-like protein - Arabidopsis thaliana N;Alternate names: protein F4P12.40 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 C;Accession: T45874 R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M. submitted to the Protein Sequence Database, January 2000 A;Reference number: 223016 A;Accession: T45874 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-228 <LIX> A;Cross-references: UNIPROT:Q9LP3; EMBL:A1132966 A;Experimental source: cultivar Columbia; BAC clone F4P12 C;Genetics: A;Map position: 3 A;Intron: 75/2; 118/3; 120/3; 145/3; 164/3; 179/3; 213/1 A;Note: F4P12.40
10	336.5	73.5	207	JC6080	transcription factor NF-Y, CCAAT-binding-like protein - Arabidopsis thaliana N;Alternate names: protein F4P12.40 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 C;Accession: T45874 R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M. submitted to the Protein Sequence Database, January 2000 A;Reference number: 223016 A;Accession: T45874 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-228 <LIX> A;Cross-references: UNIPROT:Q9LP3; EMBL:A1132966 A;Experimental source: cultivar Columbia; BAC clone F4P12 C;Genetics: A;Map position: 3 A;Intron: 75/2; 118/3; 120/3; 145/3; 164/3; 179/3; 213/1 A;Note: F4P12.40
11	336.5	73.3	186	T45874	transcription factor NF-Y, CCAAT-binding-like protein - Arabidopsis thaliana N;Alternate names: protein F4P12.40 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 C;Accession: T45874 R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M. submitted to the Protein Sequence Database, January 2000 A;Reference number: 223016 A;Accession: T45874 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-228 <LIX> A;Cross-references: UNIPROT:Q9LP3; EMBL:A1132966 A;Experimental source: cultivar Columbia; BAC clone F4P12 C;Genetics: A;Map position: 3 A;Intron: 75/2; 118/3; 120/3; 145/3; 164/3; 179/3; 213/1 A;Note: F4P12.40
12	330.5	72.0	209	S22818	transcription factor NF-Y, CCAAT-binding-like protein - Arabidopsis thaliana N;Alternate names: protein F4P12.40 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 C;Accession: T45874 R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M. submitted to the Protein Sequence Database, January 2000 A;Reference number: 223016 A;Accession: T45874 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-228 <LIX> A;Cross-references: UNIPROT:Q9LP3; EMBL:A1132966 A;Experimental source: cultivar Columbia; BAC clone F4P12 C;Genetics: A;Map position: 3 A;Intron: 75/2; 118/3; 120/3; 145/3; 164/3; 179/3; 213/1 A;Note: F4P12.40
13	325.5	70.9	160	G84919	probable CCAAT-box transcription factor protein T26F17.20
14	308.5	67.2	208	G86322	transcription factor hypothetical protein
15	288.5	62.9	144	A28123	hypothetical protein probable CCAAT-box transcription factor
16	280.5	61.1	139	C86222	transcription factor hypothetical protein
17	280.5	61.1	205	S51565	transcription factor transcription factor
18	271.5	59.2	116	S42744	transcription factor probable CCAAT-box transcription factor
19	255.5	55.7	403	E88021	protein W10D9.4 [1] transcription factor
20	230	50.1	122	S22819	DRL-like protein - TATA-binding protein
21	144.5	31.5	162	T50504	TATA-binding protein TBP-binding protein
22	144.5	31.0	159	S53502	TATA-binding protein TBP-binding protein
23	137	29.8	175	JCS365	probable transcription factor hypothetical protein hypothetical protein probable dna bindi
24	136	29.6	176	A43320	archaeal histone H
25	119	25.9	161	T40194	hypothetical prote
26	117	25.5	275	C84673	archaeal histone -
27	94.5	20.6	184	T22529	archaeal histone -
28	85.5	18.6	210	T40359	histone-related pro
29	79.5	17.3	72	A69292	histone Hmfl (impoo maltodextrin phosph
					glycogen phosphorylase channel pr
					calcium voltage-dependent
					voltage-dependent
					calcium channel pr
					voltage-dependent
					voltage-dependent
					hypothetical prote

Query Match 88.8%; Score 407.5; DB 2; Length 228;
 Best Local Similarity 80.2%; Pred. No. 8.6e-46; Indels 4; Gaps 9; Matches 81; Conservative 4; Mismatches 9; Indels 7; Gaps 1;

Db 1 RSDQDRFLPANIANSRIMKALPANGXXXXXIAKDAKCTKOCVSRISFTSEASKC 60
 28 RSDQDRFLPANIANSRIMKALPANGK-----TAKDAKTBMOBCVSFVSEASDKC 80

Oy 61 QEKRKRTINGDDLIWAMATLGFDYIEPLKVLVILXXYREKEG 101
 81 QEKRKRTINGDDLIWAMATLGFDYIEPLKVLVILQYRMEG 121

RESULT 3

E84810 hypothetical protein At2g38880 [imported] - *Arabidopsis thaliana*
 C;Keywords: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: E84810
 Rlin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayan, L.; Tailon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.; Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: E84810
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-138 <STOP>
 A;Cross-references: UNIPROT:Q9S1G0; GB:AE002093; NID:9328076; PIDN:AACT79602.1; GSPDB:GN
 C;Genetics:
 C;Gene: At2g38880
 A;Map position: 2
 C;Superfamily: transcription factor HAP3

Query Match 88.3%; Score 405.5; DB 2; Length 138;
 Best Local Similarity 80.0%; Pred. No. 9.1e-46; Indels 4; Gaps 7; Matches 80; Conservative 4; Mismatches 9; Indels 7; Gaps 1;

Oy 1 RSDQDRFLPANIANSRIMKALPANGXXXXXIAKDAKCTKOCVSRISFTSEASYC 60
 Db 20 RSDQDRFLPANIANSRIMKALPANGK-----TAKDAKTBMOBCVSFVSEASDKC 72

Oy 61 QEKRKRTINGDDLIWAMATLGFDYIEPLKVLVILXXYREKEG 100
 Db 73 QEKRKRTINGDDLIWAMATLGFDYIEPLKVLVILQYRMEG 112

RESULT 4

G71407 transcription factor, CCAAT-binding, chain A - *Arabidopsis thaliana*
 N;Alternative names: protein DL3310W
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 A;Variety: columba
 C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
 C;Accession: G71407
 R;Bevan, M.; Bancroft, I.; Bent, S.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzneger, T.; Pohl, T.M.; Terry, N.; Gel avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.; Nature 391, 485-488, 1998
 A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomench, ethoff, A.; Moore, T.; Jones, J.D.G.; Enaya, T.; Palme, K.; Bene, V.; Rechman, S.; Ans C.; Chalwatza, N.
 A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of *Arabidopsis thaliana*.
 A;Reference number: A71400; MUID:98121113; PMID:9461215
 A;Accession: G71407
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-161 <BEV>
 A;Cross-references: UNIPROT:O23310; GB:Z97336; NID:92244788; PIDN:CAB10233.1; PID:922448
 C;Genetics:
 C;Gene: At2g13570
 A;Map position: 4COP9-4G3845

RESULT 5

A;Note: DL3310W
 C;Superfamily: transcription factor HAP3
 C;Keywords: DNA binding; transcription regulation
 F;20-109/Domain: DNA binding #status predicted <DNA>
 Query Match 87.3%; Score 400.5; DB 2; Length 161;
 Best Local Similarity 78.2%; Pred. No. 4.9e-45; Indels 4; Gaps 11; Matches 79; Conservative 4; Mismatches 11; Indels 7; Gaps 1;

Oy 1 RSDQDRFLPANIANSRIMKALPANGXXXXXIAKDAKCTKOCVSRISFTSEASKC 60
 Db 20 RSDQDRFLPANIANSRIMKALPANGK-----TAKDAKTBMOBCVSFVSEASDKC 81

Oy 61 QEKRKRTINGDDLIWAMATLGFDYIEPLKVLVILXXYREKEG 101
 Db 73 QEKRKRTINGDDLIWAMATLGFDYIEPLKVLVILQYRMEG 113

RESULT 6

F84508 probable CCAAT-box binding transcription factor [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: F84508
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayan, L.; Tailon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.; Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: F84508
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-215 <STOP>
 A;Cross-references: UNIPROT:Q9S1T9; GB:AE002093; NID:94558662; PIDN:AAD22680.1; GSPDB:GN
 C;Genetics:
 C;Gene: At2g13570
 A;Map position: 2

Query Match Best Local Similarity 82.0%; Score 376.5; DB 2; Length 215; Matches 71; Conservative 10; Mismatches 13; Indels 7; Gaps 1;

RESULT 7

transcription factor NF-Y, CCAAT-binding, chain B - chicken

C;Species: Gallus gallus (chicken)

C;Accession: S24469

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999 submitted to the EMBL Data Library, January 1992

A;Reference number: S24469

A;Accession: S24469

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-180 <BEN>

A;Cross-references: EMBL:X59713; NID:963690; PIDN:CAA42233.1; PID:963691

C;Superfamily: transcription factor Hap3

C;Keywords: DNA binding; transcription regulation

F;51-140/Domain: DNA binding #status predicted <DNA>

Query Match 73.5%; Score 337.5; DB 2; Length 180; Best Local Similarity 67.3%; Pred. No. 1.1e-36; Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REQDRYLPANTSIRIMKALPKNGXXXXXXIADAKTXQSCVSEFISPTSBASKC 60

Db 51 REQDIYLPPLANVARIMKNAIPQTK-----IKAQKECVQCSVSEFISPTSEASRC 103

Qy 61 QXERKRKTINGDDLIWAMATLGFDYIEPLKVLYKXRE 98

Db 104 HQSKRKTINGEDILFAMSTLGFDSYVEPLKLYLQKFRE 141

RESULT 8

transcription factor NF-Y, CCAAT-binding, chain B - human

N;Alternate names: CAAr-box DNA-binding protein

C;Species: Homo sapiens (man)

C;Accession: S22817

R;Hooft van Huijsduijnen, R.; Li, X.Y.; Black, D.; Matthes, H.; Benoist, C.; Mathis, D.

R;Li, X.Y.; Mantovani, R.; van Huijsduijnen, R.H.; Andre, I.; Benoist, C.; Mathis, D.

Nucleic Acids Res. 20, 1087-1091, 1992

A;Title: Evolutionary variation of the CCAAT-binding transcription factor NF-Y.

A;Reference number: S22817

A;Accession: S22817

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-205 <LIX>

A;Cross-references: EMBL:X59710; NID:935049; PIDN:CAA42230.1; PID:935050

C;Superfamily: transcription factor Hap3

C;Keywords: DNA binding; transcription regulation

F;51-140/Domain: DNA binding #status predicted <DNA>

Query Match 73.5%; Score 337.5; DB 2; Length 205; Best Local Similarity 67.3%; Pred. No. 1.2e-36; Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REQDRYLPANTSIRIMKALPKNGXXXXXXIADAKTXQSCVSEFISPTSBASKC 60

Db 51 REQDIYLPPLANVARIMKNAIPQTK-----IKAQKECVQCSVSEFISPTSEASRC 103

Qy 61 QXERKRKTINGDDLIWAMATLGFDYIEPLKVLYKXRE 98

Db 106 HQSKRKTINGEDILFAMSTLGFDSYVEPLKLYLQKFRE 143

RESULT 9

transcription factor NF-Y, CCAAT-binding, chain B - mouse

C;Species: Mus musculus (house mouse)

C;Accession: F38245

C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004

R;Benoist, C.

R;Li, X.Y.; Hooft van Huijsduijnen, R.; Mantovani, R.; Benoist, C.; Mathis, D.

J. Biol. Chem. 267, 8984-8990, 1992

A;Title: Intron-exon organization of the NF-Y genes. Tissue-specific splicing modifies a

A;Reference number: A38245; MUID:92250488; PMID:1577736

A;Accession: F38245

A;Status: not compared with conceptual translation

A;Residues: 1-207 <LIA>

A;Cross-references: UNIPROT:P22669; GB:MB6215

R;Hooft van Huijsduijnen, R.; Li, X.Y.; Black, D.; Matthes, H.; Benoist, C.; Mathis, D.

EMBO J. 9, 3119-3127, 1990

A;Title: Co-evolution, from yeast to mouse: cDNA cloning of the two NF-Y (CP-1/CBP) subunits

A;Reference number: S12044; MUID:91006004; PMID:1698608

A;Accession: S12044

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-207 <HOO>

A;Cross-references: GB:X55316; NID:953362; PIDN:CAA39024.1; PID:953363

C;Superfamily: transcription factor Hap3

C;Keywords: alternative splicing; DNA binding; transcription regulation

Query Match 73.5%; Score 337.5; DB 2; Length 207; Best Local Similarity 67.3%; Pred. No. 1.2e-36; Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REQDRYLPANTSIRIMKALPKNGXXXXXXIADAKTXQSCVSEFISPTSBASKC 60

Db 53 REQDIYLPPLANVARIMKNAIPQTK-----IKAQKECVQCSVSEFISPTSEASRC 105

Qy 61 QXERKRKTINGDDLIWAMATLGFDYIEPLKVLYKXRE 98

Db 106 HQSKRKTINGEDILFAMSTLGFDSYVEPLKLYLQKFRE 143

RESULT 10

transcription factor, CCAAT-binding, chain A1 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Accession: A23692

R;Vuorio, T.; Maity, S.N.; de Crombrugge, B.

J. Biol. Chem. 265, 22480-22486, 1990

A;Title: Purification and molecular cloning of the "A" chain of a rat heteromeric CCAAT-A;Reference number: A23692; MUID:9103096; PMID:226139

A;Accession: A23692

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-207 <VVO>

A;Cross-references: UNIPROT:P22569; GB:M55045; GB:J05701; NID:9203352; PIDN:AAA40887.1; F;53-142/Domain: DNA binding #status predicted <DNA>

Query Match 73.5%; Score 337.5; DB 2; Length 207; Best Local Similarity 67.3%; Pred. No. 1.2e-36; Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REQDRYLPANTSIRIMKALPKNGXXXXXXIADAKTXQSCVSEFISPTSBASKC 60

Db 53 REQDIYLPPLANVARIMKNAIPQTK-----IKAQKECVQCSVSEFISPTSEASRC 105

Qy 61 QXERKRKTINGDDLIWAMATLGFDYIEPLKVLYKXRE 98

Db 106 HQSKRKTINGEDILFAMSTLGFDSYVEPLKLYLQKFRE 143

RESULT 11
 JG6080 transcription factor HAP3 - *Emericella nidulans*
 C;Species: *Emericella nidulans*, *Aspergillus nidulans*
 C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
 C;Accession: JG6080
 R;Papagiannopoulos, P.; Andrianopoulos, A.; Sharp, J.A.; Davis, M.A.; Hynes, M.J.
 Mol. Gen. Genet. 251, 412-421, 1996
 A;Title: The hapc gene of *Aspergillus nidulans* is involved in the expression of CCAAT-
 A;Reference number: JG6080; MUID:96205564; PMID:8709944
 A;Accession: JG6080
 A;Molecule type: mRNA
 A;Residues: 1-186 <PAP>
 A;Cross-references: UNIPROT:Q00735; GB:U35341; NID:91017715; PIDN: AAC49411.1; PID:910177
 C;Genetics:
 A;Gene: hapc
 A;Map position: 2
 A;Introns: 53/1; 90/1; 132/3
 C;Superfamily: transcription factor HAP3
 F/42-111/Domain: DNA binding #status predicted <DNA>

Query Match 73.3%: Score 316.5%; DB 2; Length 186;
 Best Local Similarity 66.0%; Pred. No. 1.5e-36;
 Matches 66; Conservative 13; Mismatches 14; Indels 7; Gaps 1;
 QY 1 REQRDRYPLANIANSRIMKALPKNGKXXXKXIAKDAKTXQCVSERISFTSEASXKC 60
 DB 42 KEDQRWLPANVIRNVRIMKALPKNAK-----TAKBAKECMQCVSISFTSEASXKC 94
 QY 61 QXRERKRTINGDDLIWAMATLGFDYIEPLKVLYXXREK 100
 DB 95 QERERKRTINGDDLIWAMTIGFDYIEPLKVLYXXREK 134

RESULT 12
 S22818 transcription factor NF-Y, CCAAT-binding, chain B - sea lamprey
 N;Alternate names: CAAAT-box DNA-binding protein
 C;Species: Petromyzon marinus (sea lamprey)
 C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
 C;Accession: S22818; S78116
 R;Li, X.Y.; Mantovani, R.; van Huijsduijnen, R.H.; Andre, I.; Benoist, C.; Mathis, D.
 Nucleic Acids Res. 20, 1087-1091, 1992
 A;Title: Evolutionary variation of the CCAAT-binding transcription factor NF-Y.
 A;Reference number: S22816; MUID:92195809; PMID:1549471
 A;Accession: S22818
 A;Molecule type: mRNA
 A;Residues: 1-1209 <LIX>
 A;Cross-references: UNIPROT:P25210; EMBL:X59712
 R;Benoist, C.
 submitted to the EMBL Data Library, January 1992
 A;Reference number: S78116
 A;Accession: S78116
 A;Molecule type: mRNA
 A;Residues: 1-110; 'R', 112-209 <BEN>
 A;Cross-references: EMBL:X59712; NID:964217; PIDN:CAA4223.1; PID:964218
 C;Superfamily: transcription factor HAP3
 C;Keywords: DNA binding; transcription regulation
 P/54-143/Domain: DNA binding #status predicted <DNA>

Query Match 72.0%: Score 330.5%; DB 2; Length 209;
 Best Local Similarity 66.3%; Pred. No. 1e-35; Mismatches 14; Indels 7; Gaps 1;
 Matches 65; Conservative 12; Mismatches 14; Indels 7; Gaps 1;

QY 1 REQRDRYPLANIANSRIMKALPKNGKXXXKXIAKDAKTXQCVSERISFTSEASXKC 60
 DB 54 RDRDYLPIANVIRNVRIMKALPKNAK-----TAKDAKBCVORCVSERISFTSEASRC 106
 QY 61 QXRERKRTINGDDLIWAMATLGFDYIEPLKVLYXXREK 98

107 HQEKTKTINGEDILFAMSTGFDSVTPLKQYQYRE 144

RESULT 13
 G64919 probable CCAAT-box binding transcription factor [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: G64919
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 eiss, D.; Newman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-160 <STOP>
 A;Cross-references: UNIPROT:OB2248; GB:AB002093; NID:93738293; PIDN: AAC63635.1; GSPPDB:GNK
 C;Genetics:
 A;Gene: At1g47810
 A;Map Position: 2
 C;Superfamily: transcription factor HAP3

Query Match 70.9%: Score 325.5%; DB 2; Length 160;
 Best Local Similarity 62.4%; Pred. No. 3.5e-33; Mismatches 22; Indels 7; Gaps 1;
 Matches 63; Conservative 9; Mismatches 22; Indels 7; Gaps 1;

QY 1 REQRDRYPLANIANSRIMKALPKNGKXXXKXIAKDAKTXQCVSERISFTSEASXKC 60
 DB 50 KEDQRWLPANVIRNVRIMKALPKNAK-----VSKEAKETMORCVSISFTSEASXKC 94
 QY 61 QXRERKRTINGDDLIWAMATLGFDYIEPLKVLYXXREK 101
 DB 103 HKERKRTINGDDICWAMANLGFDDYAOQLKKYRYRLEG 143

RESULT 14
 G66352 protein T26F17.20 [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: G66352
 R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Aman, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sekano, H.; Shiu, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A6141; MUID:21016719; PMID:11130712
 A;Accession: G66352
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-208 <STOP>
 A;Cross-references: UNIPROT:Q9SF08; GB:AE005172; NID:96552738; PIDN:AAF16537.1; GSPPDB:GN
 C;Genetics:
 A;Gene: T26F17.20
 A;Map position: 1

Query Match 67.2%: Score 308.5%; DB 2; Length 208;
 Best Local Similarity 56.0%; Pred. No. 8e-33; Mismatches 17; Indels 7; Gaps 1;
 Matches 56; Conservative 20; Mismatches 17; Indels 7; Gaps 1;

QY 1 REQRDRYPLANIANSRIMKALPKNGKXXXKXIAKDAKTXQCVSERISFTSEASXKC 60
 DB 28 REQRDRYPLANIANSRIMKALPKNAK-----ISDAAKETIOPCVSISFTSEASRC 80
 QY 61 QXRERKRTINGDDLIWAMATLGFDYIEPLKVLYXXREK 100

RESULT 15
A28123 transcription factor HAP3 - yeast. (*Saccharomyces cerevisiae*)
N;Alternate names: protein YBL021c; protein YBL0441
C;Species: *Saccharomyces cerevisiae*
C;Date: 10-Sep-1999 #Bequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A28123; S43937; S47575
R;Hahn, S.; Pinkham, J.; Wei, R.; Miller, R.; Gwarecht, L.
Mol. Cell. Biol. 8, 655-663, 1988
A;Title: The HAP3 regulatory locus of *Saccharomyces cerevisiae* encodes divergent overlap
A;Reference number: A93110; MUID:88174707; PMID:2832732
A;Accession: A28123
A;Molecule type: DNA
A;Residues: 1-144 <HAP>
A;Cross-references: UNIPROT: P13434; EMBL:M20318; NID:9577522; PIDN:AAA53538.1; PID:91716
R;van Dyck, L.; Pearce, D.A.; Sherman, F.
J. Biol. Chem., 269, 238-242, 1994
A;Title: PIM1 encodes a mitochondrial ATP-dependent protease that is required for mitoch
A;Reference number: S43937; MUID:94103216; PMID:8276800
A;Accession: S43937
A;Molecule type: DNA
A;Residues: 1-14 <VAN>
A;Cross-references: EMBL:X74544; NID:9453234; PIDN:CAA52633.1; PID:9453235
R;Gorfeau, A.; Jonnaius, J.L.; Purnelle, B.; Skila, J.; de Wergifosse, P.; van Dyck, L.
submitted to the Protein Sequence Database, August 1994
A;Submission number: S45745
A;Accession: S45755
A;Molecule type: DNA
A;Residues: 1-14 <GDP>
A;Cross-references: EMBL:235782; NID:9536016; PIDN:CA84840.1; PID:9536017; GSPDB:GN0000
C;Genetics:
A;Gene: SGD:HAP3; MIPS:YBL021C
A;Cross-references: SGD:S0000117; MIPS:YBL021C
A;Map position: 2L
C;Superfamily: transcription factor HAP3
C;Keywords: DNA binding; nucleus; transcription regulation
F;36-125/domain: DNA binding #status predicted <DNA>
Query Match 62.9%; Score 288.5; DB 1; Length 144;
Best Local Similarity 55.0%; Pred. No. 2.3e-30;
Matches 55; Conservative 18; Mismatches 20; Indels 7; Gaps 1;
QY 1 REQDRYPIANTSRIMKCALPKNGKXXXXXXIANDAKTXQBCVSEFTSPITBASXKC 60
Db 36 REQDRWPIINNVARMLKATLPPSAK-----VSQDAKECMQECUSELISFVTSAEBC 88
QY 61 OKEKRKTINGDDLIWAMATLGFSDYIRPLKVLYLXREKE 100
Db 89 AADKRKTINGEDILISHLHALGFENYAEVLUKLVYLAKYRQQ 128

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PT Pilgrim ML, Dubell AN, Pineda O, Yu G;
 XX DR WPI; 2004-132245/13.
 PT New transgenic plant comprising a recombinant polynucleotide of any one
 PT of more than 500 nucleotide sequences, useful in bioinformatic search
 PT methods.

XX PS Claim 1; SEQ ID NO 802; 435pp; English.

XX The invention describes a transgenic plant comprising a recombinant
 CC polynucleotide of any one of more than 500 nucleotide sequences fully
 CC defined in the specification or its complement. The method of the
 CC invention can be used to produce a plant having altered traits such as:
 CC enhanced tolerance to abiotic stress; glyophosphate tolerance; hormone
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;
 CC altered flower structure; change in stem bifurcations; altered branching
 CC pattern; reduced apical dominance; reduced trichome density; lack of
 CC trichomes; reduced ectopic trichome development; altered trichome
 CC development; increase in trichome number; altered stem morphology;
 CC increased root growth; increased root hairs; altered seed development;
 CC altered cell proliferation or cell differentiation; rapid development;
 CC premature senescence; increased necrosis; increase in seedling or plant
 CC size; decreased plant size; leaf morphology; seed morphology; seed
 CC biochemistry; increase in root anthocyanins; increase in plant
 CC anthocyanins; or alteration in light response or shade avoidance. The
 CC transgenic plant, polynucleotides and polypeptides are useful in
 CC bioinformatic search methods. This is the amino acid sequence of a plant
 CC transcription factor, and an orthologue of *Arabidopsis thaliana*.
 CC transcription factors isolated in the invention, that can be used in the
 CC creation of a transgenic plant with altered traits.

XX SQ sequence 160 AA;

Query Match 92.3%; Score 423.5; DB 8; Length 160;
 Best Local Similarity 85.1%; Pred. No. 2.2e-54; Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

Oy 1 RSDRQYPLANSRIMKKGALPKNGXXXXXXIAKDAKXTKBCVSFISFTSEASXKC 60
 Db 27 RQDRYPLANTNSRIMKKGALPKNGK----IAKDAKXTMRCVSFISFTSEASXKC 79

Oy 61 QKEKRKTINGDDILWAMATLGFDYISPLKVYLXXYRKEG 101
 Db 80 QKEKRKTINGDDILWAMATLGFDYISPLKVYLARYRAEG 120

RESULT 2

ADS16959
 ID ADS16959 standard; protein; 160 AA.
 XX AC ADS16959;
 XX DT 02-DEC-2004 (first entry)
 XX DB Plant polypeptide #18.
 XX
 KW Abiotic stress tolerance; LIL-related CCAAT transcription factor;
 KW B domain; heat tolerance; drought stress tolerance; cold tolerance;
 KW salt stress tolerance; MYB-related transcription factor;
 KW seedling germination.
 OS Undentified.

XX PN WO2004076638-A2.
 XX PD 10-SEP-2004.
 XX PP 25-FEB-2004; 2004WO-US005654.
 PR 25-FEB-2003; 2003US-00374780.
 PR 30-SEP-2003; 2003US-00675852.

PA (MEND-) MENDEL BIOTECHNOLOGY INC.
 XX PI Sherman BK, Riechmann JL, Ratcliffe O, Jiang C, Heard JE,
 PI Haake V, Creelman RA, Adam LJ, Reuber LT, Keddie JS, Dubell AN;
 PI Pineda O, Repetti PE, Century KS, Gutierrez NI, Yu G, Broun PE;
 PI Kumamoto RW, Pilgrim ML;
 XX DR WPI; 2004-653405/63.

XX PT New transgenic plant having increased abiotic stress tolerance as
 PT compared to non-transgenic plants of the same species, useful in
 PT bioinformatic research methods.

XX Disclosure; Fig 10; 297pp; English.

CC The invention relates to a transgenic plant having increased abiotic
 CC stress tolerance as compared to non-transgenic plants of the same
 CC species, where the transgenic plant comprises in its genome a transgene
 CC encoding a polypeptide member of the G482 subclade of the non-LC1-like
 CC clade of proteins of the LIL-related CCAAT transcription factor family,
 CC where overexpression of the polypeptide member confers abiotic stress
 CC tolerance. The invention also relates to a seed from the transgenic
 CC plant, a method for producing a transgenic plant having increased
 CC tolerance to abiotic stress comprising providing an expression vector
 CC comprising the polynucleotide sequence encoding the polypeptide, and
 CC regulatory elements operably linked to the nucleotide sequence, where the
 CC regulatory elements are effective to control expression of the nucleotide
 CC sequence in a target plant, introducing the expression vector into a
 CC plant cell, growing the plant cell, allowing the plant to overexpress the
 CC polypeptide and identifying one or more abiotic stress tolerant plants so
 CC produced by comparing the one or more abiotic stress tolerant plants with
 CC one or more non-transgenic plants of the same species, and a method for
 CC increasing a plant's tolerance to abiotic stress comprising providing the
 CC vector cited above and transforming the target plant with the vector to
 CC generate a transformed plant with increased tolerance to abiotic stress,
 CC compared to non-transgenic plants of the same species. The transgenic
 CC plant comprises a polypeptide comprising a B domain. The B domain binds
 CC to DNA at a transcription-regulating region comprising the motif CCAAT,
 CC where the binding regulates transcription of the DNA. The regulation of
 CC transcription confers increased abiotic stress tolerance in the
 CC transgenic plant as compared to non-transgenic plants of the same
 CC species. The abiotic stress tolerance is selected from heat tolerance,
 CC drought stress tolerance, cold tolerance and salt stress tolerance. The
 CC transgenic plant further comprises a constitutive, inducible, or tissue-
 CC specific promoter operably linked to the recombinant polynucleotide. The
 CC recombinant polynucleotide is incorporated into an expression vector
 CC comprising one or more regulatory elements that are effective to control
 CC expression of the recombinant polynucleotide in a target plant. The
 CC transgenic plant is a cultured host cell. The transgenic plant can
 CC comprise in its genome a transgene encoding a polypeptide member of the
 CC MYB-related transcription factor family, where overexpression of the
 CC polypeptide member confers abiotic stress tolerance. The transgenic plant
 CC is useful in bioinformatic research methods. The invention provides
 CC transgenic plants with improved seedling germination and performance
 CC under conditions of limited nitrogen. This sequence represents a
 CC polypeptide used in the scope of the invention.

XX SQ sequence 160 AA;

Query Match 92.3%; Score 423.5; DB 8; Length 160;
 Best Local Similarity 85.1%; Pred. No. 2.2e-54; Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

Oy 1 RSDRQYPLANSRIMKKGALPKNGXXXXXXIAKDAKXTKBCVSFISFTSEASXKC 60
 Db 27 RQDRYPLANTNSRIMKKGALPKNGK----IAKDAKXTMRCVSFISFTSEASXKC 79

Oy 61 QKEKRKTINGDDILWAMATLGFDYISPLKVYLXXYRKEG 101
 Do 80 QKEKRKTINGDDILWAMATLGFDYISPLKVYLARYRAEG 120

RESULT 3

ADO63706
ID ADO63706 standard; protein; 173 AA.
XX
AC ADO63706;
XX DT 15-JUL-2004 (first entry)
XX DB Transcription factor G3471 orthologous sequence, SEQ ID 2173.
XX KW plant; transcription factor; transgenic plant; abiotic stress tolerance;
KW osmotic stress tolerance; cold tolerance; heat tolerance;
KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
KW glyphosate resistance; flowering; fertility; seed development.
OS Glycine max.
XX PN WO2004031349-A2.
XX PD 15-APR-2004.
XX PP 18-SEP-2003; 2003WO-US030292.
XX PR 18-SEP-2002; 2002US-0411837P.
XX PR 17-DEC-2002; 2002US-0434165P.
PR 24-APR-2003; 2003US-0465809P.
XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.
XX PT Jiang C., Heard JB., Ratcliffe O., Creelman RA., Adam LJ., Reuber TL.;
PT Riechmann JL., Hake V., Dubell AN., Keddie JS., Sherman BK.;
DR N-PSDB; ADO63705.
XX PT New recombinant polynucleotide encoding transcription factor
PT polypeptides, useful for producing transgenic plants with advantageous
PT properties compared to a reference plant.
XX Disclosure; SEQ ID NO 2173; 510pp; English.
XX PS The present invention relates to novel plant transcription factor
CC proteins (I), and nucleotide sequences (II) (ADO6154-ADO63770). The
CC sequences can be used to produce transgenic plantS, which overexpress
CC (II), where the transgenic plant has an altered trait as compared to a
non-transgenic plant or wild-type plant. The transgenic plant comprises
an altered trait selected from increased tolerance to abiotic stress,
increased tolerance to osmotic stress, increased tolerance to cold,
increased germination in cold, increased tolerance to heat, increased
germination in heat, increased tolerance to freezing conditions,
increased tolerance to low nitrogen conditions, increased tolerance to
low phosphate conditions, increased tolerance to disease, including
fungal disease and particularly *Bryosiphon*, *Fusarium* and *Botryotinia*,
increased tolerance to multiple fungal pathogens, increased resistance to
glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
increased sensitivity to ACC, altered sugar sensing, increased tolerance
to sugars, altered carbon/nitrogen sensing, early flowering, late
flowering, altered flower structure, loss of flower determinacy, reduced
fertility, altered shoot meristem development, altered branching pattern,
altered stem morphology, altered vascular tissue structure, reduced
apical dominance, altered trichome density, altered trichome development,
altered trichome structure, altered root development, altered shade
avoidance, altered seed development, altered seed ripening, altered seed
germination, slow growth, fast growth, altered cell differentiation,
altered cell proliferation, altered cell expansion, altered phase change,
altered senescence, abnormal embryo development, altered programmed cell
death, lethality when overexpressed, altered necrosis patterns, increased
plant size, increased biomass, large seedlings, dwarfed plants, dark
green leaves, change in leaf shape, increased leaf size and mass, light
green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
altered seed coloration, altered seed size, altered seed shape, large
seed, increased leaf wax, increased leaf fatty acids, altered seed oil
content, altered seed protein content, altered seed prenyl lipid content,
altered leaf prenyl lipid content, increased anthocyanin levels, and
altered leaf prenyl lipid content, increased anthocyanin levels, and

CC decreased anthocyanin levels. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 173 AA;

RESULT 4
ADS16957
ID ADS16957 standard; protein; 173 AA.
XX AC ADS16957;
XX DT 02-DEC-2004 (first entry)
XX DB Plant polypeptide #16.
XX KW Abiotic stress tolerance; IIL-related CCAT transcription factor;
KW B domain; heat tolerance; drought stress tolerance; cold tolerance;
KW salt stress tolerance; MYB-related transcription factor;
KW seedling germination.
XX OS Undeclared.
XX PN WO2004076638-A2.
XX PD 10-SEP-2004.
XX PR 25-FEB-2004; 2004WO-US005654.
XX PR 30-SEP-2003; 2003US-00374780.
XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.
XX PT Sherman BK., Riechmann JL., Ratcliffe O., Jiang C., Heard JB.,
PT Hake V., Creelman RA., Adam LJ., Reuber TL., Keddie JS., Dubell AN.,
PT O., Repetti PP., Century KS., Gutierrez NI., Yu G., Broun PE.,
PT Kumimoto RW., Pilgrim ML.;
XX DR WPI; 2004-653405/63.
XX PT New transgenic plant having increased abiotic stress tolerance as
PT compared to non-transgenic plants of the same species, useful in
PT bioinformatic research methods.
XX PS Disclosure; Fig 10; 297pp; English.
XX The invention relates to a transgenic plant having increased abiotic
CC stress tolerance as compared to non-transgenic plants of the same
CC species, where the transgenic plant comprises in its genome a transgene
CC encoding a polypeptide member of the G482 subclade of the non-LBC1-like
CC clade of proteins of the LIL-related CCAT transcription factor family,
CC where overexpression of the polypeptide member confers abiotic stress
CC tolerance. The invention also relates to a seed from the transgenic
CC plant, a method for producing a transgenic plant having increased
CC tolerance to abiotic stress comprising providing an expression vector
CC comprising the polynucleotide sequence encoding the polypeptide, and
CC regulatory elements operably linked to the nucleotide sequence, where the
regulatory elements are effective to control expression of the nucleotide

sequence in a target plant, introducing the expression vector into a plant cell, growing the plant cell, allowing the plant to overexpress the polypeptide and identifying one or more abiotic stress tolerant plants so produced by comparing the one or more abiotic stress tolerant plants with one or more non-transgenic plants of the same species, and a method for increasing a plant's tolerance to abiotic stress comprising providing the vector cited above and transforming the target plant with the vector to generate a transformed plant with increased tolerance to abiotic stress, compared to non-transgenic plants of the same species. The transgenic plant comprises a polypeptide comprising a B domain. The B domain binds to DNA at a transcription-regulating region comprising the motif CCAAT where the binding regulates transcription of the DNA. The regulation of transcription confers increased abiotic stress tolerance in the transgenic plant as compared to non-transgenic plants of the same species. The abiotic stress tolerance is selected from heat tolerance, drought stress tolerance, cold tolerance and salt stress tolerance. The transgenic plant further comprises a constitutive, inducible, or tissue-specific promoter operably linked to the recombinant polynucleotide. The recombinant polynucleotide is incorporated into an expression vector comprising one or more regulatory elements that are effective to control expression of the recombinant polynucleotide in a target plant. The transgenic plant is a cultured host cell. The transgenic plant can comprise in its genome a transgene encoding a polypeptide member of the M2B-related transcription factor family, where overexpression of the polypeptide member confers abiotic stress tolerance. The transgenic plant is useful in bioinformatic research methods. The invention provides transgenic plants with improved seedling germination and performance under conditions of limited nitrogen. This sequence represents a polypeptide used in the scope of the invention.

SQ Sequence 173 AA;

Query Match Best Local Similarity 92.3%; Score 423.5; DB 8; Length 173;

Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

Oy 1 RSDRDRYPIANISRMKMKALPKNGKXXXXXKIAKDAKXTKCVSFSRISFTSEASKC 60
 Db 26 RSDRDRYPIANISRMKMKALPKNGK-----IAKDAKDTMOCVSPISFTSEASKC 78
 Oy 61 QKEKRKTINGDDLIWAMATLGFDYIPLKVYLARYRAEG 101
 Db 79 QKEKRKTINGDDLIWAMATLGFDYIPLKVYLARYRAEG 119

RESULT 5
ADO63718 ID ADO63718 standard; protein; 174 AA.AC ADO63718;
XX DT 15-JUL-2004 (first entry)

XX Transcription factor G3477 orthologous sequence, SEQ ID 2185.

XX Plant; transcription factor; transgenic plant; abiotic stress tolerance; KW osmotic stress tolerance; cold tolerance; heat tolerance; KW low nitrogen tolerance; low phosphate tolerance; fungal disease; KW glyphosate resistance; flowering; fertility; seed development. OS Glycine max.

XX XX WO2004031349-A2.
PD 15-APR-2004.

PF 18-SEP-2003; 2003WO-US030292.
XX PR 18-SEP-2002; 2002US-0411837P.
PR 17-DEC-2002; 2002US-0434165P.
PR 24-APR-2003; 2003US-0465809P.
XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.

XX

Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL; PI Riechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK;

PR DR WPI; 2004-330163/30.

DR N-PSDB; ADO63717.

DR N-PSDB; ADO63717.

DR N-PSDB; ADO63717.

New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.

Disclosure: SEQ ID NO 2185; 510pp; English.

The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO6134-AD063778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to multiple fungal pathogens, increased resistance to cold, increased germination in heat, increased tolerance to heat, increased germination in heat, increased tolerance to freezing conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to disease, including fungal disease and particularly *Erysiphe*, *Fusarium* and *Botrytis*, increased tolerance to multiple fungal pathogens, increased resistance to glycosidase, increased sensitivity to ABA, reduced sensitivity to ABA, increased sensitivity to ACC, altered sugar sensing, increased tolerance to sugars, altered carbon/nitrogen sensing, early flowering, late flowering, altered flower structure, loss of flower determinacy, reduced fertility, altered shoot meristem development, altered branching pattern, altered stem morphology, altered vascular tissue structure, reduced apical dominance, altered trichome density, altered trichome development, altered trichome structure, altered root development, altered shade avoidance, altered seed development, altered seed ripening, altered seed germination, slow growth, fast growth, altered cell differentiation, altered cell proliferation, altered cell expansion, altered phase change, altered senescence, abnormal embryo development, altered programmed cell death, lethality when overexpressed, altered necrosis patterns, increased plant size, increased biomass, large seedlings, dwarfed plants, dark green leaves, change in leaf shape, increased leaf size and mass, light green or gray leaves, glossy leaves, altered abaxial/adaxial polarity, altered seed coloration, altered seed size, altered seed shape, large seed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed protein content, increased seed protein content, decreased anthocyanin levels. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

SQ Sequence 174 AA;

Query Match Best Local Similarity 85.1%; Score 423.5; DB 8; Length 174;

Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

Oy 1 RSDRDRYPIANISRMKMKALPKNGKXXXXXKIAKDAKXTKCVSFSRISFTSEASKC 60
 Db 27 RSDRDRYPIANISRMKMKALPKNGK-----IAKDAKDTMOCVSPISFTSEASKC 79

Oy 61 QKEKRKTINGDDLIWAMATLGFDYIPLKVYLARYRAEG 101
 Db 80 QKEKRKTINGDDLIWAMATLGFDYIPLKVYLARYRAEG 120

RESULT 6
ADO63704 ID ADO63704 standard; protein; 174 AA.

AC ADO63704;

DT 15-JUL-2004 (first entry)

XX
DB Transcription factor G3470 orthologous sequence, SEQ ID 211.
XX
KW Plant; transcription factor; transgenic plant; abiotic stress tolerance;
KW osmotic stress tolerance; cold tolerance; heat tolerance;
KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
KW glyphosate resistance; flowering; fertility; seed development.
OS Glycine max.
XX
PN WO2004031349-A2.
PD 15-APR-2004.
XX
PR 16-SEP-2003; 2003WO-US030292.
PR 18-SEP-2002; 2002US-0011837P.
PR 17-DEC-2002; 2002US-0034165P.
PR 24-APR-2003; 2003US-0465809P.
XX
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
PT New recombinant polynucleotide encoding transcription factor
PT polypeptides, useful for producing transgenic plants with advantageous
PT properties compared to a reference plant.
XX
CC Disclosure; SEQ ID NO 2171; 510pp; English.
PS
XX
CC The present invention relates to novel plant transcription factor
CC proteins (I) and nucleotide sequences (II) (AD061534-AD063778). The
CC sequences can be used to produce transgenic plants, which overexpress
CC (II), where the transgenic plant has an altered trait as compared to a
non-transgenic plant or wild-type plant. The transgenic plant comprise
an altered trait selected from increased tolerance to abiotic stress,
increased tolerance to osmotic stress, increased tolerance to cold,
increased germination in cold, increased tolerance to heat, increased
germination in heat, increased tolerance to freezing conditions,
increased tolerance to low nitrogen conditions, increased tolerance to
low phosphate conditions, increased tolerance to disease, including
fungal disease and particularly *Bryosiphon*, *Rusarium* and *Botryosphaeria*,
increased tolerance to multiple fungal pathogens, increased resistance to
glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
increased sensitivity to ACC, altered sugar sensing, increased tolerance
to sugars, altered carbon/nitrogen sensing, early flowering, late
flowering, altered flower structure, loss of flower determinacy, reduced
fertility, altered shoot meristem development, altered branching pattern,
altered stem morphology, altered vascular tissue structure, reduced
apical dominance, altered trichome density, altered trichome development,
altered trichome structure, altered root development, altered shade
avoidance, altered seed development, altered seed ripening, altered seed
germination, low growth, fast growth, altered cell differentiation,
altered cell proliferation, altered cell expansion, altered phase change,
altered senescence, abnormal embryo development, altered programmed cell
death, lethality when overexpressed, altered necrosis patterns, increased
plant size, increased biomass, large seedlings, dwarfed plants, dark
green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
altered seed coloration, altered seed size, altered seed shape, large
seed, increased leaf wax, increased leaf fatty acids, altered seed oil
content, altered seed protein content, altered secoiridoid content,
altered leaf phenyl lipid content, increased anthocyanin levels, and
decreased anthocyanin levels. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
electronic format directly from WIPO at
http://wipo.int/pub/published_pct_sequences.
XX
Sequence 174 AA;

Query Match 92.3%; Score 423.5; DB 9; Length 174;
Best Local Similarity 85.1%; Pred. No. 2.5e-54; Mismatches 8; Indels 7; Gaps 1;
Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

QY	1 RHDQRYPLANISRMKVKALPKAPEGXXXXXKARDAKTKQCVSEISIFSEASWIC 60
Db	27 RQDQYPLANISRMKVKALPKAPEGK-----TAKDAKTMQSCVSEISIFSEASWIC 79
QY	61 QXERKRKTINGDDLWAMATLGFDSDYIEPLKUVLXKXRHEG 101
Db	80 QXERKRKTINGDDLWAMATLGFDSDYIEPLKVLKIRKAG 120

RESULT 7
ADS16958
ID ADS16958 standard; protein; 174 AA.
XX
AC ADS16958;
XX
DE 02-DEC-2004 (first entry)
Plant polypeptide #17.
XX
KW Abiotic stress tolerance; IIL-related CCAAT transcription factor;
KW B domain; heat tolerance; drought stress tolerance; cold tolerance;
KW salt stress tolerance; MYB-related transcription factor;
KW seedling germination.

XX
OS Unidentified.
XX
PN WO2004076638-A2.
PD 10-SEP-2004.
XX
PR 25-FEB-2004; 2004WO-US005654.
PR 25-FEB-2003; 2003US-00374780.
PR 30-SEP-2003; 2003US-00675852.
XX
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
PT Sherman BK, Riechmann JL, Ratcliffe O, Jiang C, Heard JB,
PI Haake V, Creelman RA, Adam LJ, Reuber LT, Keddie JS, Duell AN,
PI Pineda O, Repetti PP, Century KS, Gutierrez NI, Yu G, Broun PE,
PI Kumimoto RW, Pilgrim ML;
DR WIPO; 2004-653405/63.
XX
PT New transgenic plant having increased abiotic stress tolerance as
PT compared to non-transgenic plants of the same species, useful in
bioinformatic research methods.
XX
PS Disclosure; Fig 10; 297pp; English.
The invention relates to a transgenic plant having increased abiotic
stress tolerance as compared to non-transgenic plants of the same
species, where the transgenic plant comprises in its genome a transgene
encoding a polypeptide member of the G482 subclade of the non-LEC1-like
clade of protein of the LIL-related CCAAT transcription factor family,
where overexpression of the polypeptide member confers abiotic stress
tolerance. The invention also relates to a seed from the transgenic
plant, a method for producing a transgenic plant having increased
tolerance to abiotic stress comprising providing an expression vector
comprising the polynucleotide sequence encoding the polypeptide, and
regulatory elements operably linked to the nucleotide sequence, where the
regulatory elements are effective to control expression of the nucleotide
sequence in a target plant, introducing the expression vector into a
plant cell, growing the plant cell, allowing the plant to overexpress the
polypeptide and identifying one or more abiotic stress tolerant plants so
produced by comparing the one or more abiotic stress tolerant plants with
one or more non-transgenic plant of the same species, and a method for
increasing a plant's tolerance to abiotic stress comprising providing the

CC vector cited above and transforming the target plant with the vector to
 CC generate a transformed plant with increased tolerance to abiotic stress,
 CC compared to non-transgenic plants of the same species. The transgenic
 CC plant comprises a polypeptide comprising a B domain. The B domain binds
 CC to DNA at a transcription-regulating region comprising the motif CCAAT
 CC transcription confers increased abiotic stress tolerance in the
 CC transgenic plant as compared to non-transgenic plants of the same
 CC species. The abiotic stress tolerance is selected from heat tolerance,
 CC drought stress tolerance, cold tolerance and salt stress tolerance. The
 CC transgenic plant further comprises a constitutive, inducible, or tissue-
 CC specific promoter operably linked to the recombinant polynucleotide. The
 CC recombinant polynucleotide is incorporated into an expression vector
 CC comprising one or more regulatory elements that are effective to control
 CC expression of the recombinant polynucleotide in a target plant. The
 CC transgenic plant is a cultured host cell. The transgenic plant can
 CC comprise in its genome a transgene encoding a polypeptide member of the
 CC MYB-related transcription factor family, where overexpression of the
 CC polypeptide member confers abiotic stress tolerance. The transgenic plant
 CC is useful in bioinformatic research methods. The invention provides
 CC transgenic plants with improved seedling germination and performance
 CC under conditions of limited nitrogen. This sequence represents a
 XX polypeptide used in the scope of the invention.

SQ Sequence 174 AA;

Query Match 92.3%; Score 423.5; DB 8; Length 174;
 Best Local Similarity 85.1%; Pred. No. 2.5e-54; Mismatches 8; Indels 7; Gaps 1;
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

OY 1 RSDRDRYPLTANSRIMKKA[PANGKXXXXXXIAKDAKDTXKOCVSRISFTSEASXKC 60
 27 RSDRDRYPLTANSRIMKKA[PANGK----IAKDAKDTXKOCVSRISFTSEASXKC 79

OY 61 QKEKRKTINGDDLLWAMATLGFSDYIPLKVKVLXXREXEG 101

Db 80 QKEKRKTINGDDLLWAMATLGFSDYIPLKVKVLARYREAG 120

RESULT 8

ABG70264 standard; protein; 178 AA.
 ID ABG70264;

AC ABG70264;

DT 21-OCT-2002 (first entry)

XX DE LBC-I-related transcription factor polypeptide #17.

XX KW Maize; balsam pear; eucalyptus; rice; soybean; bread wheat; plant;
 KW leafy cotyledon-related transcription factor; plant embryogenesis;
 KW LBCI-related transcription factor; thale cress; plant breeding.

XX OS Zea maya.

XX PN WO200257439-A2.

XX PD 25-JUL-2002.

XX PR 24-OCT-2001; 2001WO-US050908.

XX PR 24-OCT-2000; 2000US-0242739P.

XX PR (DUPO) DU PONT DE NEMOURS & CO E I.

XX PA (DUPO) PIONEER HI-BRED INT INC.

XX PI Allen SM, Allen WB, Cahoon RE, Spelbaum S, Pamodu OO, Harvell LT;
 Jones TU, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
 Tarczynski MC;

XX DR WPI; 2003-201509/19.

XX PR Novel nucleotide fragment encoding polypeptides having receptor-like
 PT protein kinase activity; calmodulin-like activity, useful for altering oil
 PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.

XX PS Claim 12; Page 451; 542pp; English.

PT The present invention describes an isolated nucleotide fragment (1)
 PT manipulation of plant growth.

XX Example 3; Fig 1; 63pp; English.

XX PS The invention relates to a polypeptide with leafy cotyledon1 (LECI)-related transcription factor activity and its associated polynucleotide. The sequences are useful in facilitating studies for better understanding of plant embryogenesis, and providing genetic tools for the manipulation of plant growth. All or a substantial portion of the polynucleotides are useful as probes for genetically and physically mapping the genes that they are a part of, and as marker for traits linked to the genes, which are useful in plant breeding to develop lines with desired phenotypes. The probes may also be used in direct fluorescence in situ hybridisation mapping. Sequences ABG70268-ABG70267 represent LECI-related transcription factor polypeptides of the invention

SQ Sequence 178 AA;

Query Match 91.0%; Score 417.5; DB 5; Length 178;
 Best Local Similarity 83.2%; Pred. No. 2e-53; Mismatches 8; Indels 7; Gaps 1;
 Matches 84; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

OY 1 RSDRDRYPLTANSRIMKKA[PANGKXXXXXXIAKDAKDTXKOCVSRISFTSEASXKC 60
 30 RSDRDRYPLTANSRIMKKA[PANGK----IAKDAKDTXKOCVSRISFTSEASXKC 82

Db 61 QKEKRKTINGDDLLWAMATLGFSDYIPLKVKVLXXREXEG 101

ID ABR40821
 ID ABR40821 standard; protein; 178 AA.

XX AC ABR40821;

XX DT 16-MAY-2003 (first entry)

XX DS Zea maya oil trait related protein sequence SEQ ID NO:413.

XX Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; oil; receptor-like protein kinase; mitogen activated protein kinase; oil; LIP15-like transcription factor; caleosin; ATP citrate lyase; SNFL; CRC-like transcription factor; antisense inhibition; co-suppression; transgenic plant.

XX OS Zea maya.

XX PN WO200302751-A2.

XX PD 09-JAN-2003.

XX PR 27-JUN-2002; 2002WO-US020152.

XX PR 29-JUN-2001; 2001US-0301913P.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Allen SM, Allen WB, Cahoon RE, Spelbaum S, Pamodu OO, Harvell LT;
 Jones TU, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
 Tarczynski MC;

XX DR WPI; 2003-201509/19.

XX PR Novel nucleotide fragment encoding polypeptides having receptor-like
 PT protein kinase activity; calmodulin-like activity, useful for altering oil
 PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.

XX PS Claim 12; Page 451; 542pp; English.

CC The present invention describes an isolated nucleic acid sequence (NS) chosen from a NS encoding a

CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
 CC activated protein (MAP)-kinase activity, LIP1-like transcription factor
 CC activity, calmodulin-like activity, ATP citrate lyase activity, SNP-like
 CC activity and CKC-like transcription factor activity. Also described: (1)
 CC complement (II); (2) a chimeric construct (III) comprising (I) or
 CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
 CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
 CC oil obtained from (V). (I) or its part can be used in antisense
 CC inhibition or co-suppression in a transformed plant. (III) is useful for
 CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
 CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
 CC creating transgenic plants having altered lipid profiles. (I) can also be
 CC used as a hybridisation probe. ACC00626 to ACC0868 and ABR41591 to
 CC ABR40879 represent sequences used in the exemplification of the present
 CC invention

XX

SQ Sequence 178 AA;

Query Match 91.0%; Score 417.5; DB 6; Length 178;
 Best Local Similarity 83.2%; Pred. No. 2e-53; Matches 8; Mismatches 2; Indels 7; Gaps 1;
 Matches 84; Conservative 2;

Oy 1 REQRKRTINGDDLIWAMATLGFDYIEPLKVLYLXXYREXEG 60
 Db 30 REQDRFLPLANISRMKKAIPANGK-----IAKDAKETVOCVSEFISPTISEASDKC 82

Oy 61 OXERKRKTTINGDDLIWAMATLGFDYIEPLKVLYLXXYREXEG 101
 Db 83 OREKRKTTINGDDLIWAMATLGFDYIEPLKVLYLQKYREMEG 123

RESULT 10
 ADI42322 ID ADI42322 standard; protein; 178 AA.

XX AC ADI42322;

XX DT 22-APR-2004 (first entry)

XX XX

DB Plant transcription factor #302.

XX XX

KW transgenic; plant; enhanced tolerance to abiotic stress;
 KW glyophosphate tolerance; hormone sensitivity; disease resistance;
 KW sugar sensing; flowering; flower structure; stem bifurcation;
 KW branching pattern; apical dominance; trichome; stem morphology;
 KW root growth; root hair; seed development; cell proliferation;
 KW cell differentiation; premature senescence; necrosis; plant size;
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;
 KW transcription factor; gene; db.

OS Zea mayes.

PN US2004119927-A1.

XX

PD 29-JAN-2004.

XX

PP 25-FEB-2003; 2003US-00374780.

XX

PR 18-APR-2001; 2001US-00837944.

XX

PA (SHER/) SHERMAN B K.
 PA (RIEC/) RIECHMANN J L.
 PA (JIAN/) JIANG C.
 PA (HEAR/) HEARD J B.
 PA (HAAK/) HAAKE V.
 PA (CREE/) CRESLMAN R A.
 PA (RATC/) RATCLIFFE O.
 PA (ADAM/) ADAM L J.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN P B.
 PA (PILG/) PILGRIM M L.

PA (DOBE/) DUBEILL A N.
 PA (PINB/) PINEDA O.
 PA (TUGG/) YU G.

XX

PT Sherman BK, Riechmann JL, Jiang C, Heard JB, Haake V,
 PT Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE,
 PT Pilgrim ML, Dubell AN, Pineda O, Yu G;

XX DR WPI; 2004-132245/13.

XX New transgenic plant comprising a recombinant polynucleotide of any one
 PT of more than 500 nucleotide sequences, useful in bioinformatic search
 PT methods.

XX

PS Claim 1; SEQ ID NO 785; 435pp; English.

XX

CC The invention describes a transgenic plant comprising a recombinant
 CC polynucleotide of any one of more than 500 nucleotide sequences fully
 CC defined in the specification or its complement. The method of the
 CC invention can be used to produce a plant having altered traits such as:
 CC enhanced tolerance to abiotic stress; glyophosphate tolerance; hormone
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;
 CC altered flower structure; change in stem bifurcations; altered branching
 CC pattern; reduced apical dominance; reduced trichome density; lack of
 CC trichomes; reduced ectopic trichome development; altered stem morphology;
 CC increased root growth; increased root hairs; altered seed development;
 CC altered cell proliferation or cell differentiation; rapid development;
 CC premature senescence; increased necrosis; increase in seedling or plant
 CC size; decreased plant size; leaf morphology; seed morphology; seed
 CC biochemistry; increase in root anthocyanins; increase in plant
 CC anthocyanins; or alteration in light response or shade avoidance. The
 CC transgenic plant, polynucleotides and polypeptides are useful in
 CC bioinformatic search methods. This is the amino acid sequence of a plant
 CC transcription factor isolated in the invention, that can be used in the
 CC creation of a transgenic plant with altered traits.

XX

SQ Sequence 178 AA;

Query Match 91.0%; Score 417.5; DB 8; Length 178;
 Best Local Similarity 83.2%; Pred. No. 2e-53; Matches 8; Mismatches 2; Indels 7; Gaps 1;
 Matches 84; Conservative 2;

Oy 1 REQRKRTINGDDLIWAMATLGFDYIEPLKVLYLXXYREXEG 60
 Db 30 REQDRFLPLANISRMKKAIPANGK-----IAKDAKETVOCVSEFISPTISEASDKC 82

Oy 61 OXERKRKTTINGDDLIWAMATLGFDYIEPLKVLYLXXYREXEG 101
 Db 83 OREKRKTTINGDDLIWAMATLGFDYIEPLKVLYLQKYREMEG 123

RESULT 11
 ADI42323 ID ADI42323 standard; protein; 179 AA.

XX AC ADI42323;

XX DT 22-APR-2004 (first entry)

XX XX

DB Plant transcription factor #303.

XX XX

KW transgenic; plant; enhanced tolerance to abiotic stress; disease resistance;
 KW glyophosphate tolerance; hormone sensitivity; stem bifurcation;
 KW sugar sensing; flowering; flower structure; trichome; stem morphology;
 KW branching pattern; apical dominance; root growth; root hair; seed development; cell proliferation;
 KW cell differentiation; premature senescence; necrosis; plant size;
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;
 KW transcription factor; gene; db.

XX			PR	18-JUN-1999;	99US-0139462P.
AC	AAG04651;		PR	18-JUN-1999;	99US-0139463P.
XX			PR	18-JUN-1999;	99US-0139750P.
XX			DE	Arabidopsis thaliana	protein fragment SEQ ID NO: 757.
XX			DB		
KW	Protein identification; signal transduction pathway; metabolic pathway;		PR	22-JUN-1999;	99US-0139891P.
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		PR	23-JUN-1999;	99US-0140355P.
KW	termination sequence.		PR	23-JUN-1999;	99US-0140695P.
XX			PR	24-JUN-1999;	99US-0140823P.
OS	Arabidopsis thaliana.		PR	28-JUN-1999;	99US-0140991P.
XX			PR	30-JUN-1999;	99US-0141287P.
PN	BP1033405-A2.		PR	01-JUL-1999;	99US-0141842P.
XX			PR	01-JUL-1999;	99US-0142152P.
PD	06-SEP-2000.		PR	02-JUL-1999;	99US-0142052P.
XX			PR	06-JUL-1999;	99US-0142390P.
PF	25-FEB-2000; 2000EP-00301439.		PR	08-JUL-1999;	99US-0142803P.
XX			PR	09-JUL-1999;	99US-0142920P.
PR	25-FEB-1999;	99US-0121823P.	PR	12-JUL-1999;	99US-0142977P.
PR	05-MAR-1999;	99US-0123180P.	PR	13-JUL-1999;	99US-0143542P.
PR	03-MAR-1999;	99US-0123548P.	PR	14-JUL-1999;	99US-0143624P.
PR	23-MAR-1999;	99US-0125788P.	PR	15-JUL-1999;	99US-0144005P.
PR	25-MAR-1999;	99US-0126261P.	PR	16-JUL-1999;	99US-0144055P.
PR	29-MAR-1999;	99US-0126783P.	PR	16-JUL-1999;	99US-0144086P.
PR	01-APR-1999;	99US-0127462P.	PR	19-JUL-1999;	99US-0144323P.
PR	06-APR-1999;	99US-0128234P.	PR	19-JUL-1999;	99US-0144332P.
PR	08-APR-1999;	99US-0128714P.	PR	19-JUL-1999;	99US-0144333P.
PR	16-APR-1999;	99US-0129845P.	PR	19-JUL-1999;	99US-0144344P.
PR	19-APR-1999;	99US-0130077P.	PR	19-JUL-1999;	99US-0144355P.
PR	21-APR-1999;	99US-0130443P.	PR	20-JUL-1999;	99US-0144359P.
PR	23-APR-1999;	99US-0130501P.	PR	20-JUL-1999;	99US-0144632P.
PR	23-APR-1999;	99US-013091P.	PR	20-JUL-1999;	99US-0144884P.
PR	28-APR-1999;	99US-0131443P.	PR	21-JUL-1999;	99US-0144814P.
PR	30-APR-1999;	99US-0132048P.	PR	21-JUL-1999;	99US-0144915P.
PR	30-APR-1999;	99US-0132407P.	PR	21-JUL-1999;	99US-0145066P.
PR	04-MAY-1999;	99US-0132484P.	PR	21-JUL-1999;	99US-0145089P.
PR	05-MAY-1999;	99US-0132485P.	PR	22-JUL-1999;	99US-0145087P.
PR	06-MAY-1999;	99US-0132486P.	PR	22-JUL-1999;	99US-0145099P.
PR	06-MAY-1999;	99US-0132487P.	PR	22-JUL-1999;	99US-0145193P.
PR	07-MAY-1999;	99US-0132863P.	PR	23-JUL-1999;	99US-0145145P.
PR	11-MAY-1999;	99US-0132864P.	PR	23-JUL-1999;	99US-0145218P.
PR	14-MAY-1999;	99US-0134218P.	PR	23-JUL-1999;	99US-0145224P.
PR	14-MAY-1999;	99US-0134219P.	PR	26-JUL-1999;	99US-0145276P.
PR	14-MAY-1999;	99US-0134221P.	PR	27-JUL-1999;	99US-0145913P.
PR	18-MAY-1999;	99US-0134763P.	PR	27-JUL-1999;	99US-0145918P.
PR	18-MAY-1999;	99US-0134941P.	PR	27-JUL-1999;	99US-0145919P.
PR	20-MAY-1999;	99US-0135144P.	PR	28-JUL-1999;	99US-0145951P.
PR	21-MAY-1999;	99US-0135353P.	PR	03-AUG-1999;	99US-0146386P.
PR	24-MAY-1999;	99US-0135421P.	PR	02-AUG-1999;	99US-0146388P.
PR	25-MAY-1999;	99US-0135629P.	PR	02-AUG-1999;	99US-0163699P.
PR	27-MAY-1999;	99US-0136392P.	PR	03-AUG-1999;	99US-0147038P.
PR	28-MAY-1999;	99US-0136393P.	PR	04-AUG-1999;	99US-0147204P.
PR	01-JUN-1999;	99US-0137223P.	PR	04-AUG-1999;	99US-0147302P.
PR	03-JUN-1999;	99US-0137528P.	PR	05-AUG-1999;	99US-0147122P.
PR	04-JUN-1999;	99US-0137502P.	PR	05-AUG-1999;	99US-0147260P.
PR	07-JUN-1999;	99US-0137724P.	PR	06-AUG-1999;	99US-0173032P.
PR	08-JUN-1999;	99US-0138034P.	PR	06-AUG-1999;	99US-0147416P.
PR	10-JUN-1999;	99US-0138540P.	PR	09-AUG-1999;	99US-0147433P.
PR	10-JUN-1999;	99US-0138841P.	PR	09-AUG-1999;	99US-0147935P.
PR	14-JUN-1999;	99US-0139119P.	PR	10-AUG-1999;	99US-0148117P.
PR	18-JUN-1999;	99US-0139456P.	PR	11-AUG-1999;	99US-0148319P.
PR	16-JUN-1999;	99US-0139452P.	PR	12-AUG-1999;	99US-0133121P.
PR	18-JUN-1999;	99US-0139453P.	PR	13-AUG-1999;	99US-0148555P.
PR	18-JUN-1999;	99US-0139459P.	PR	13-AUG-1999;	99US-0148684P.
PR	18-JUN-1999;	99US-0139460P.	PR	15-AUG-1999;	99US-0149168P.
PR	18-JUN-1999;	99US-0139455P.	PR	17-AUG-1999;	99US-0149155P.
PR	18-JUN-1999;	99US-0139456P.	PR	18-AUG-1999;	99US-0149462P.
PR	18-JUN-1999;	99US-0139452P.	PR	20-AUG-1999;	99US-0149722P.
PR	18-JUN-1999;	99US-0139453P.	PR	20-AUG-1999;	99US-0149939P.
PR	18-JUN-1999;	99US-0139459P.	PR	20-AUG-1999;	99US-0149902P.
PR	18-JUN-1999;	99US-0139461P.	PR	23-AUG-1999;	99US-0149930P.

PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-015084P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151080P.
 PR 31-AUG-1999; 99US-0151303P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 10-SEP-1999; 99US-0152363P.
 PR 13-SEP-1999; 99US-0153070P.
 PR 15-SEP-1999; 99US-0153788P.
 PR 16-SEP-1999; 99US-0154018P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 23-SEP-1999; 99US-0155139P.
 PR 24-SEP-1999; 99US-0155486P.
 PR 29-SEP-1999; 99US-0155639P.
 PR 04-OCT-1999; 99US-0156566P.
 PR 05-OCT-1999; 99US-0157733P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158028P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 14-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159328P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159848P.
 PR 21-OCT-1999; 99US-0160711P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 26-OCT-1999; 99US-0161355P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 28-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
 PR 28-OCT-1999; 99US-0162142P.

Query Match 90.3%; Score 414.5; DB 3; Length 141;
 Best Local Similarity 81.2%; Pred. No. 4.1e-53; Mismatches 9; Indels 7; Gaps 1;
 Matches 82; Conservative 3;

Oy 1 REQDRYIPIANISRIMKALPKNGXXXXXXXXXAKDACKTXQCVSERISFTSEASXKC 60
 Db 20 REQDRYIPIANISRIMKALPKNG-----IGKDAKDVTQBCVSFISFTSEASDKC 72

Oy 61 QXERKRKTINGDDLIWAMATLGFDYIEPLKVLYXXREXEG 101
 Db 73 QKERKRKTINGDDLIWAMATLGFDYIEPLKVLYARYRELEG 113

RESULT 14
 ADE37175
 ID ADE37175 standard; protein: 141 AA.
 XX
 AC ADB37175;
 XX

DT 29-JAN-2004 (first entry)
 XX
 DB Plant yield related protein from clone G481.
 XX
 KW transcription factor; tolerance; environmental condition;
 KW microbial disease; fungal disease; viral disease; pest infestation;
 KW herbicide sensitivity; heavy metal tolerance; heavy metal uptake;
 KW growth improvement; photocondition; nutrient uptake; hormone sensitivity;
 KW transgenic plant.
 XX
 OS *Arabidopsis thaliana*.
 PN MO2003014327-A2.
 XX
 PD 20-FEB-2003.
 XX
 PF 09-AUG-2002; 2002WO-US026966.
 XX
 PR 09-AUG-2001; 2001US-0310847P.
 PR 19-NOV-2001; 2001US-0336049P.
 PR 11-DEC-2001; 2001US-0338592P.
 PR 14-JUN-2002; 2002US-00171468.
 XX
 PA (NEND-) MENDEL BIOTECHNOLOGY INC.
 XX
 PR Reuber TL, Riechmann JL, Heard JE, Jiang C, Adam LJ, Dubell AN;
 PR Ratcliffe O, Pineda O, Yu GL, Broun PS;
 XX
 DR WPI; 2003-256576/25.
 N-PSDB; AD337174.

XX
 PS Disclosure; SEQ ID NO 114; 470pp; English.
 XX
 The invention relates to a number of cDNA sequence and their encoded proteins which are especially transcription factor cDNAs and their proteins. The isolated or recombinant polynucleotide is useful for producing a modified plant with a modified trait, e.g. enhanced tolerance to environmental conditions, improved tolerance to microbial, fungal or viral diseases, improved tolerance to pest infestation, decreased herbicide sensitivity, improved tolerance of heavy metals, or enhanced ability to take up heavy metals, improved growth under poor photoconditions, improved nutrient uptake, or reduced hormone sensitivity. The transgenic plants are useful for growing a progeny plant comprising the desired trait. The polynucleotides and polypeptides are also useful in bioinformatic search methods. This sequence represents one of the proteins of the invention.

SQ Sequence 141 AA;

Query Match 90.3%; Score 414.5; DB 7; Length 141;
 Best Local Similarity 81.2%; Pred. No. 4.1e-53; Mismatches 9; Indels 7; Gaps 1;
 Matches 82; Conservative 3;

Oy 1 REQDRYIPIANISRIMKALPKNGXXXXXXXXXAKDACKTXQCVSERISFTSEASXKC 60
 Db 20 REQDRYIPIANISRIMKALPKNG-----IGKDAKDVTQBCVSFISFTSEASDKC 72

Oy 61 QXERKRKTINGDDLIWAMATLGFDYIEPLKVLYXXREXEG 101
 Db 73 QKERKRKTINGDDLIWAMATLGFDYIEPLKVLYARYRELEG 113

RESULT 15
 ADF50740
 ID ADF50740 standard; protein: 141 AA.
 XX
 AC ADF50740;
 XX

DT 12-FEB-2004 (first entry)
 XX
 DB Thale cress transcription factor G481 protein.
 KW thale cress; transgenic; transcription factor; G481; abiotic;
 KW biotic stress; drought; secondary metabolite; storage nutrient; sterol;
 KW starch; leaf; flower; senescence.
 XX OS *Arabidopsis thaliana*.
 XX
 PN US2003188330-A1.
 XX
 PD 02-OCT-2003.
 XX
 PP 18-MAR-2002; 2002US-00112887.
 PR 18-MAR-2002; 2002US-00112887.
 PA (HEAR/) HEARD J.
 XX PT Heard J;
 XX DR WRI; 2003-811784/76.
 XX N-PSDB; ADF50739.
 XX
 PT Transgenic Plants with altered traits e.g. resistance to stress or
 PT increased oil content, contain recombinant DNA encoding specific
 transcription factors.
 XX
 PS Claim 4; SEQ ID NO 2; 39pp; English.
 XX
 CC This invention relates to novel genes for phenotypically modifying a
 CC plant using transgenesis. Specifically, it comprises a recombinant
 CC polynucleotide encoding a transcription factor having an altered trait
 CC compared with the wild-type plant and hence exhibiting an altered
 CC phenotype or expressing an altered level of at least one gene associated
 CC with a plant trait. The present invention describes two novel
 CC transcription factors, identified as G481 and G1466 from *Arabidopsis*
 CC *thaliana* that provide altered phenotypic traits when over-expressed in
 CC the seed of transgenic plants. A wide range of traits can be modified
 CC using these transcription factors and related antisense molecules to
 CC alter the plant's properties including tolerance of abiotic or biotic
 CC stress e.g. from drought or viral infection, production of secondary
 CC metabolites and storage nutrients e.g. starch, vitamins or sterols; and
 CC also the physical characteristics and growth can be altered to change for
 CC example leaf and flower senescence. This polypeptide sequence is the
 CC *Arabidopsis thaliana* G481 protein of the invention.
 XX
 SQ Sequence 141 AA;
 Query Match 90.3%; Score 414.5; DB 7; length 141;
 Best Local Similarity 81.2%; Pred. No. 4.1e-53;
 Matches 82; Conservative 3; Mismatches 9; Indels 7; Gaps 1;
 Ov 1 REBDYRLPANIISRIMKGQALPKXGXXXXXXAAKDAKCKTXCVCUSERISPTSEASKC 60
 Db 20 REBDYRLPANIISRIMKGQALPK-----IGDAKDTVQCSVSERISPTSEASDKC 72
 Ov 61 QKERRKRTKINGDDIILWAMATLGFRDYIEPLKVLYKXYREKEG 101
 Db 73 QKERRKRTKIVNGDDIILWAMATLGFFDYLEPLKIVLARYRELEG 113

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Gencore version 5.1.6

Om protein - protein search, using SW model

Run on: November 17, 2005, 08:43:04 ; Search time 168 seconds

(without alignments)

30.7.857 Million cell updates/sec

Title: US-10-678-588a-8

perfect score: 459

Sequence: 1 REQDRYLIPIANISRIMKAL.....FEDVIEPLKVLYXREXEG 101

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03;*

1: uniprot_sprot;*

2: uniprot_trembl;*

- Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	417.5	91.0	167	2	Q84NF0
2	417.5	91.0	179	1	CBF4 MAIZE
3	414.5	90.3	141	3	Q8LGO0
4	407.5	88.8	176	2	057KJ2
5	407.5	88.8	228	2	09LF13
6	402.5	87.7	173	2	08VY4K
7	400.5	87.3	161	2	023310
8	395.5	86.2	187	2	026334
9	395.5	86.2	190	2	09GF13
10	393.5	85.7	178	2	09ZQ03
11	388.5	84.6	152	2	084VF3
12	388.5	84.6	178	2	08AFL1
13	388.5	84.6	189	2	08SITB
14	388.5	84.6	224	2	069U40
15	386.5	84.2	219	2	05VNL1
16	386.5	84.2	219	2	075127
17	376.5	82.0	143	2	084NB9
18	376.5	82.0	215	2	08SITB
19	366.5	79.8	241	2	065KK1
20	366.5	79.8	290	2	06VNU0
21	338.5	73.7	78	2	084k78
22	338.5	73.7	204	2	096WPO
23	337.5	73.5	148	2	063091
24	337.5	73.5	151	1	CBFA CHICK
25	337.5	73.5	159	2	Q9D056
26	337.5	73.5	202	2	06WVJ9
27	337.5	73.5	206	2	06T2f0
28	337.5	73.5	207	1	CBFA_HUMAN
29	337.5	73.5	207	1	CBFA_MOUSE
30	337.5	73.5	207	1	CBFA RAT
31	337.5	73.5	207	2	Q6RG77

RESULT 1

Q8ANFO

OBANFO

Q8ANFO

Q8ANFO;

DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DB CCAAT-binding transcription factor subunit A (CBF-A) (NF-Y protein chain B) (NF-YB) (CAT-box DNA binding protein subunit B).
 GN Name=Nf-y2;
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OC NCBI_TaxID=4577;
 RP [1] SQUENCE FROM N.A.
 RX MEDLINE=9215809; PubMed=1549471;
 RA Li X.-Y., Mantovani R., Hooft van Huijsduijnen R., Andre I., Benoit C., Mathis D.;
 RT "Evolutionary variation of the CCAAT-binding transcription factor NF-Y";
 RL Nucleic Acids Res. 20:1087-1091 (1992).
 CC -I- FUNCTION: Stimulates the transcription of various genes by recognizing and binding a CCAAT motif in promoters, for example in type I collagen, albumin and beta-actin genes.
 CC -I- SUBUNIT: Heterotrimeric transcription factor composed of three components, A, B and C. NF-YB and NF-YC must interact and dimerize for NF-YA association and DNA binding.
 CC -I- SUBCELLULAR LOCATION: Nuclear.
 CC -I- DOMAIN: Can be divided into three domains: the weakly conserved A domain, the highly conserved B domain thought to be involved in subunit interaction and DNA binding, and the Glu-rich C domain.
 CC -I- SIMILARITY: Belongs to the CBF-A subunit family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X59714; CAM42234.1; -. [6]
 DR PR; 622820; 822820.
 DR HSP; P25208; INI.J.
 DR TRANSFAC; T05212; -. [7]
 DR MatzDB; 6928; -. [8]
 DR InterPro; IPR003956; CBFA_NFYB.
 DR InterPro; IPR003558; CBFA_NFYB_domain.
 DR InterPro; IPR003957; CBFA_NFYB_topis.
 DR InterPro; IPR007124; Hist_TAR.
 DR InterPro; IPR009072; Histone-fold.
 DR Pfam; PF00808; CBD_NFYB_HMF; 1.
 DR PRINTS; PR00015; CCAATSUBUNTA.
 DR PROSITE; PS00685; CBFA_NFYB; 1.
 KW Activator; DNA-binding; Nuclear protein; Transcription regulation.
 FT DOMAIN 1 29 A domain.
 FT DOMAIN 30 119 B domain.
 FT DOMAIN 120 179 C domain.
 FT DNA BIND 36 42 BY Similarity.
 SQ SEQUENCE 179 AA; 18995 MW; 30621316CE69454 CRC64;

Query Match, Best Local Similarity 91.0%; Score 417.5; DB 1, Length 179;
 Matches 84; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

OY 1 REQRKTIQDNLWAMATGFEDYIEPLKLYXREEG 101
 QY 61 QERKRKTINDDLWAMATGFEDYIEPLKLYXREEG 101
 Db 30 REQRKTIQDNLWAMATGFEDYIEPLKLYXREEG 123

OSIAGO
 ID OSIAGO PRELIMINARY; PRT; 141 AA.
 AC OSIAGO_023633;
 DT 01-MAY-2000 (TREMBREL. 13, Created)
 DT 01-JUN-2002 (TREMBREL. 21, Last sequence update)
 DT 05-JUN-2004 (TREMBREL. 27, Last annotation update)
 DB Putative CCAAT-binding transcription factor subunit (transcription factor).
 GN Name=Ar2g3880; Synonyms=hap3a;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; audicoryledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 RN [1] NCBI_TaxID=3702;
 RN
 RP SQUENCE FROM N.A.
 RA Rounsbury S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M., Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C., RUL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SQUENCE FROM N.A.
 RA Town C.D., Kaul S.;
 RA Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SQUENCE FROM N.A.
 RA Rewards D., Smith A.G., Murray J.A.;
 RA Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SQUENCE FROM N.A.
 RA MEDLINE=22088475; PubMed=12093376;
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RA "Full-length messenger RNA sequences greatly improve genome annotation.", Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).
 RN [5]
 RP SQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.;
 RA Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SQUENCE FROM N.A.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Huan V.W., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C., Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kawaji J., Kim C.J., Naruoka M., Nguyen M., Palm C.J., Sakurai T., Sakai M., Seki M., Shin P., Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Becker J.R., Theologis A.;
 RA Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP SQUENCE FROM N.A.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Huan V.W., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C., Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kawaji J., Kim C.J., Naruoka M., Nguyen M., Palm C.J., Sakurai T., Sakai M., Seki M., Shin P., Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Becker J.R., Theologis A.;
 RA Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AAC0570; AAC79602.2; -. [8]
 DR EMBL; Y13723; CAM4231.1; -. [9]
 DR EMBL; AX08854; RAM66086.1; -. [10]
 DR EMBL; BT004266; AAQ4266.1; -. [11]
 DR EMBL; BT005536; AAQ63956.1; -. [12]
 DR PIR; E84810; E84810.
 DR HSP; P25208; INI.J.
 DR TRANSFAC; T05198; -. [13]
 DR EMBL; Y13723; CAM4231.1; -. [14]
 DR GO; GO_0005634; C-nucleus; IEA.
 DR GO; GO_003677; F-DNA binding; IEA.
 DR GO; GO_0006355; P-regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003956; CBFA_NFYB.

RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
 RA Bowser L., Carninci P., Chang S., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P.,
 RA Hayashizaki Y., Shinozaki K., Davis R.W., Theologis A.,
 RA Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AY07077; AML49943.1; --.
 DR EMBL; AY091673; AML10272.1; --.
 DR HSSP; P25208; INI.U.
 DR GO; GO:0005334; C:nucleus; IEA.
 DR GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
 DR PFAM; PF00808; CBPF_NFYB_HMP; 1.
 DR PRINTS; PRO00615; CCAATSUBUNTA.
 DR PROSITE; PS00685; CBPA_NFYB; 1.
 SQ SEQUENCE 173 AA, 18598 MW, 8C01E135B2DBC36A CRC64;
 Query Match 87.7%; Score 402.5; DB 2; Length 173;
 Best Local Similarity 79.2%; Pred. No. 1.3e-43; Pdb
 Matches 80; Conservative 4; Mismatches 10; Indels 7; Gaps 1;
 DR HSSP; P25208; INI.U.
 DR TRANSAC; T05340; --.
 DR GO; GO:0005334; C:nucleus; IEA.
 DR GO; GO:0003677; P:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003956; CBFA_NFYB.
 DR InterPro; IPR003558; CBFA_NFYB domain.
 DR InterPro; IPR003957; CBFA_NFYB topics.
 DR InterPro; IPR009072; Histone-fold.
 DR InterPro; IPR007124; Hist-TAF.
 DR PFAM; PF00808; CBPF_NFYB_HMP; 1.
 DR PRINTS; PRO00615; CCAATSUBUNTA.
 DR PROSITE; PS00685; CBPA_NFYB; 1.
 SQ SEQUENCE 161 AA, 17186 MW, 5C452B22D98A7AF4 CRC64;
 Query Match 87.3%; Score 400.5; DB 2; Length 161;
 Best Local Similarity 78.2%; Pred. No. 3.3e-43; Pdb
 Matches 79; Conservative 4; Mismatches 11; Indels 7; Gaps 1;
 DR HSSP; P25208; INI.U.
 DR TRANSAC; T05340; --.
 DR GO; GO:0005334; C:nucleus; IEA.
 DR GO; GO:0003677; P:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003956; CBFA_NFYB.
 DR InterPro; IPR003558; CBFA_NFYB domain.
 DR InterPro; IPR003957; CBFA_NFYB topics.
 DR InterPro; IPR009072; Histone-fold.
 DR InterPro; IPR007124; Hist-TAF.
 DR PFAM; PF00808; CBPF_NFYB_HMP; 1.
 DR PRINTS; PRO00615; CCAATSUBUNTA.
 DR PROSITE; PS00685; CBPA_NFYB; 1.
 SQ SEQUENCE FROM N.A.
 ID 023310 PRELIMINARY; PRT; 161 AA.
 AC 023310;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DB CCAT-binding transcription factor subunit A (CBF-A) (Putative CCAAT-
 DB binding transcription factor subunit A (CBF-A)) (At4g14540).
 OS Name=d3310w, Synonyms=At4g14540, Atg14540/d13310w;
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 [1] R
 SEQUENCE FROM N.A.
 RA Bayan M., Stilekema W., Murphy G., Wanbutt R., Pohl T., Terryn N.,
 RA Kreis M., Kavanagh T., Entian K.D., Rieger M., James R., Obermaier B., Dueserhoff A.,
 RA Puigdomenech P., Hatzopoulos P., Obermaier B., Dueserhoff A.,
 RA Jones J., Palme K., Anorgate W., Delseny M., Bancroft I., Mewes H.W.,
 RA Schueler C., Chalwatzie N.,
 RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
 [2] R
 SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 RN R
 SEQUENCE FROM N.A.
 DR HSSP; P25208; INI.U.
 DR TRANSAC; T05195; --.
 DR GO; GO:0005334; C:nucleus; IEA.
 DR GO; GO:0003677; P:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003556; CBPA_NFYB.
 DR InterPro; IPR003558; CBPA_NFYB domain.
 DR InterPro; IPR003557; CBPA_NFYB topics.
 DR InterPro; IPR009072; Histone-fold.
 DR InterPro; IPR007124; Hist-TAF.
 DR PFAM; PF00808; CBPF_NFYB_HMP; 1.
 DR PRINTS; PRO00615; CCAATSUBUNTA.
 DR PROSITE; PS00685; CBPA_NFYB; 1.
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Heuan V.W.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
 RA Submitted (FEBB-2003) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; Z97336; CAB10233.1; --.
 DR EMBL; AL161539; CBAB78496.1; --.
 DR EMBL; AXL1818; BAC42460.1; --.
 DR EMBL; BT003684; AAO3912.1; --.
 DR PIR; GT1407; GT1407.
 DR HSSP; P25208; INI.U.
 DR TRANSAC; T05340; --.
 DR GO; GO:0005334; C:nucleus; IEA.
 DR GO; GO:0003677; P:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003956; CBFA_NFYB.
 DR InterPro; IPR003558; CBFA_NFYB domain.
 DR InterPro; IPR003957; CBFA_NFYB topics.
 DR InterPro; IPR009072; Histone-fold.
 DR InterPro; IPR007124; Hist-TAF.
 DR PFAM; PF00808; CBPF_NFYB_HMP; 1.
 DR PRINTS; PRO00615; CCAATSUBUNTA.
 DR PROSITE; PS00685; CBPA_NFYB; 1.
 SQ SEQUENCE 161 AA, 17186 MW, 5C452B22D98A7AF4 CRC64;
 Query Match 87.3%; Score 400.5; DB 2; Length 161;
 Best Local Similarity 78.2%; Pred. No. 3.3e-43; Pdb
 Matches 79; Conservative 4; Mismatches 11; Indels 7; Gaps 1;
 DR HSSP; P25208; INI.U.
 DR TRANSAC; T05340; --.
 DR GO; GO:0005334; C:nucleus; IEA.
 DR GO; GO:0003677; P:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003956; CBFA_NFYB.
 DR InterPro; IPR003558; CBFA_NFYB domain.
 DR InterPro; IPR003957; CBFA_NFYB topics.
 DR InterPro; IPR009072; Histone-fold.
 DR InterPro; IPR007124; Hist-TAF.
 DR PFAM; PF00808; CBPF_NFYB_HMP; 1.
 DR PRINTS; PRO00615; CCAATSUBUNTA.
 DR PROSITE; PS00685; CBPA_NFYB; 1.

DR	InterPro; IPR003958; CBFA_NFYB_domain.
DR	InterPro; IPR003957; CBFA_NFYB_topis.
OS	Oryza sativa (Japonica cultivar-group).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	Embryophytes; Oryzeae; Oryza.
OX	NCBI_TaxID:39947;
RN	[1] SEQUENCE FROM N.A.
RX	MEDLINE=2311120; PubMed=14750518; DOI=10.1023/B:PLMN.0000007001.30865.0F;
RA	Cooper B., Hutchinson D., Park S., Guimil S., Luginbuhl P., Ellero C., Goff S.A., Glazebrook J., Park S., Guimil S., Luginbuhl P., Ellero C., RT "Identification of rice (<i>Oryza sativa</i>) proteins linked to the cyclin-mediated regulation of the cell cycle."; Plant Mol. Biol. 53:273-279(2003).
RL	Plant Mol. Biol. 53:273-279(2003).
DR	EMBL; AV224530; AR072650.1; -.
DR	HSSP; P25208; INIJ.
DR	Gramene; Q8AVP3; -.
DR	GO; GO:0005634; C:nucleus; IEA.
DR	GO; GO:000677; F:DNA binding; IEA.
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR	InterPro; IPR003956; CBFA_NFYB domain.
DR	InterPro; IPR003957; CBFA_NFYB_topis.
DR	InterPro; IPR003958; CBFA_NFYB_topis.
DR	InterPro; IPR003959; CBFA_NFYB_topis.
DR	InterPro; IPR003960; CBFA_NFYB_topis.
DR	InterPro; IPR003961; CBFA_NFYB_topis.
DR	InterPro; IPR003962; Histone-fold.
DR	InterPro; IPR07124; Hist-TAF.
DR	Pfam; PF0008; CBFD_NFYB_HMF; 1.
DR	PRINTS; PRO0615; CCATSUBUNTA.
DR	PROSITE; PRO0685; CCATA domain.
DR	PROSITE; PRO0685; CBFA_NFYB; 1.
DR	SEQUENCE 178 AA; 19200 MW; ID620383B9B82926 CRC64;
SQ	Query Match 84.6%; Score 388.5; DB 2; Length 178; Best Local Similarity 83.2%; Pred. No. 1.1e-41; Matches 79; Conservative 1; Mismatches 8; Indels 7; Gaps 1;
QY	1 REDDRYPIANASRIMKALPANGKXXXXXXIAKADKTCRKCVSFISFTSEASKC 60
Db	33 REQDRFLPIANSRIMKALPANGK-----IAKADKETLQBCVSFSRISFTSEADKC 85
QY	61 QSKERKTTNGDILIWAMATLGFDYIPEPLKVLYKXYREXEG 101
Db	86 QKERRKTINGDILIWAMATLGFDYIPEPLKVLYKXYREMEG 126
RN	[2] SEQUENCE FROM N.A.
ID	Q81TB
AC	Q81TB
DT	01-JUN-2002 (TREMBrel. 21; Created)
DT	01-JUN-2002 (TREMBrel. 21; Last sequence update)
DT	25-OCT-2004 (TREMBrel. 28; Last annotation update)
DE	Putative CAAAT-box DNA binding protein (CCAAT-binding protein).
GN	Name=P056812.4; Synonyms=CIBI, P0460C04-24;
OS	Oryza sativa (Japonica cultivar-group).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	Embryophytes; Oryzeae; Oryza.
OX	NCBI_TaxID:39947;
RN	[1] SEQUENCE FROM N.A.
RX	PUBMED=12447438; DOI=10.1038/nature0184;
RA	Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., RA Hosokawa S., Masukawa M., Arikawa K., Choden Y., Hayashi M., RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., RA Hishishita S., Honda M., Ichikawa Y., Idouma A., Iijima M., Ikeda M., RA Ikeno M., Ichoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K., RA Karasawa W., Katogiri S., Kikuta A., Kobayashi N., Kono I., RA Machita K., Maekawa T., Mizuno H., Mizubayashi T., Mukai Y., RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., RA Namiki N., Negishi M., Ohta I., Ono N., Seiji S., Sakai, K., Shibata M., RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terashawa K., Tsuji K., RA Waki K., Yamagata H., Yamane H., Yoshihara R., Yukawa K., RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Sun M.Y., RA Yano M., Jiang J., Gotohori T.; RT "The genome sequence and structure of rice chromosome 1."; RT Nature 420:312-316 (2002).
RN	[2] SEQUENCE FROM N.A.
RP	Yao Q., Peng R., Xiong A./ Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AP003211; BAB9732.1; -.
DR	EMBL; AP004366; BAB9231.1; -.
DR	EMBL; AV332466; AAQ01152.1; -.
DR	P25208; INIJ.
DR	Gramene; Q81TB; -.
DR	GO; GO:0005634; C:nucleus; IEA.
DR	GO; GO:0005634; F:DNA binding; IEA.
DR	GO; GO:0005635; P:regulation of transcription, DNA-dependent; IEA.
DR	InterPro; IPR003956; CBFA_NFYB.
DR	InterPro; IPR003957; CBFA_NFYB_topis.
DR	InterPro; IPR003958; CBFA_NFYB_topis.
DR	InterPro; IPR003959; CBFA_NFYB_topis.
DR	InterPro; IPR003960; CBFA_NFYB_topis.
DR	InterPro; IPR003961; CBFA_NFYB_topis.
DR	InterPro; IPR003962; Histone-fold.
DR	InterPro; IPR07124; Hist-TAF.
DR	Pfam; PF0008; CBFD_NFYB_HMF; 1.

DR PRINTS; PR00615; CCAATSUBUNTA.
 DR PROSITE; PS00685; CBPA_NPYB; 1.
 SQ SEQUENCE 189 AA; 20752 MW; 0D385703DACS25D3 CRC64;
 Query Match 84.6%; Score 388.5; DB 2; Length 189;
 Best Local Similarity 75.2%; Pred. No. 1.4e-41; Indels 7; Gaps 1;
 Matches 76; Conservative 7; Mismatches 9; Indels 7; Gaps 1;
 Qy 1 REQDRYPLIANSRIMKALPANGXXXXXXTAKDAKTXQCVSERISFTSEASKC 60
 Db 19 REQDRYPLIANSRIMKALPANG-----ISDAKETVQCVSERISFTGASDKC 71
 Qy 61 OXERKRKTNGDDLIWAMATLGFDYIEPKVLYXXREXEG 101
 Db 72 OXERKRKTNGEDLIPAWGTTGFFEVDPKLKHYKREMEG 112
 RESULT 14
 Q9J40 PRELIMINARY; PRT; 224 AA.
 ID Q9J40 AC 069J40 DT 25-OCT-2004 (Tremblel. 28, Created)
 DT 25-OCT-2004 (Tremblel. 28, Last sequence update)
 DT 25-OCT-2004 (Tremblel. 28, Last annotation update)
 DE Putative transcription factor.
 GN Name=OSUNBA0072106.11; Synonyms=P0493C06.26;
 OS Oryza sativa (Indica cultivar-group).
 OC Isikaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TAXID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TR64;
 RC X-Z.; Knush G.S., Bennett J.;
 RL Submitted (Nov-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AX062181; AXA47206.1; -.
 DR HSPB; P19267; IANW.
 DR GO; GO_000534; C:nucleus; IEA.
 DR GO; GO_0003677; P:DNA binding; IEA.
 DR GO; GO_0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003556; CBPA_NPYB.
 DR InterPro; IPR003558; CBPA_NPYB_domain.
 DR InterPro; IPR003557; CBPA_NPYB_topis.
 DR InterPro; IPR00972; Histone-fold.
 DR InterPro; IPR007124; Hist_TAF.
 PRAM; PP00808; CBPD_NPYB_HMP; 1.
 DR PRINTS; PR00615; CCAATSUBUNTA.
 DR PROSITE; PS00685; CBPA_NPYB; 1.
 SQ SEQUENCE 219 AA; 22987 MW; 704BD8B9E0C5F2C0 CRC64;
 Query Match 84.2%; Score 386.5; DB 2; Length 219;
 Best Local Similarity 75.2%; Pred. No. 2.9e-41; Indels 7; Gaps 1;
 Matches 76; Conservative 6; Mismatches 12; Indels 7; Gaps 1;
 Qy 1 REQDRYPLIANSRIMKALPANGXXXXXXTAKDAKTXQCVSERISFTSEASKC 60
 Db 23 REQDRYPLIANSRIMKALPANG-----ISDAKETVQCVSERISFTGASDKC 75
 Qy 61 OXERKRKTNGDDLIWAMATLGFDYIEPKVLYXXREXEG 101
 Db 76 OXERKRKTNGDDLIWAMATLGFDYIEPKVLYXXREXEG 116
 Search completed: November 17, 2005, 08:55:33
 Job time : 170 secs
 Query Match 84.6%; Score 388.5; DB 2; Length 224;
 Best Local Similarity 75.2%; Pred. No. 1.5e-41; Indels 7; Gaps 1;
 Matches 76; Conservative 7; Mismatches 11; Indels 7; Gaps 1;
 Qy 1 REQDRYPLIANSRIMKALPANGXXXXXXTAKDAKTXQCVSERISFTSEASKC 60
 Db 21 REQDRYPLIANSRIMKALPANG-----ISDAKETVQCVSERISFTGASDKC 73
 Qy 61 OXERKRKTNGDDLIWAMATLGFDYIEPKVLYXXREXEG 101
 Db 74 OXERKRKTNGDDLIWAMATLGFDYIEPKVLYXXREXEG 114
 RESULT 15
 QSYNKL



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OM protein - protein search, using sw model
 Run on: November 17, 2005, 08:46:10 ; Search time 25 Seconds
 (without alignments)
 301.582 Million cell updates/sec

Title: US-10-678-588A-8
 perfect score: 459
 Sequence: 1 REQDRYPLPANISRIMKAL.....FEDVYIEPLKVLYKXYREXEG 101

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Parents AA:
 1: /cgmn2_6/ptodata/1/iaa/5A_COMB.pep: *
 2: /cgmn2_6/ptodata/1/iaa/5B_COMB.pep: *
 3: /cgmn2_6/ptodata/1/iaa/6A_COMB.pep: *
 4: /cgmn2_6/ptodata/1/iaa/6B_COMB.pep: *
 5: /cgmn2_6/ptodata/1/iaa/PCUTS_COMB.pep: *
 6: /cgmn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	402.5	87.7	90	3	US-09-103-478-20 Sequence 20, Appl
2	402.5	87.7	90	3	US-09-193-931C-20 Sequence 20, Appl
3	402.5	87.7	90	4	US-09-510-052-30 Sequence 30, Appl
4	401.5	87.5	218	4	US-09-828-302-23 Sequence 23, Appl
5	397.5	86.5	219	4	US-09-540-211A-1051 Sequence 1051, Appl
6	337.5	73.5	207	4	US-09-530-092-1008 Sequence 1008, Appl
7	337.5	73.5	211	4	US-09-943-016-7348 Sequence 7348, Appl
8	332.5	72.4	90	3	US-09-103-478-21 Sequence 21, Appl
9	332.5	72.4	90	3	US-09-103-478-24 Sequence 24, Appl
10	332.5	72.4	90	3	US-09-103-478-25 Sequence 25, Appl
11	332.5	72.4	90	3	US-09-193-931C-21 Sequence 21, Appl
12	332.5	72.4	90	3	US-09-193-931C-24 Sequence 24, Appl
13	332.5	72.4	90	3	US-09-193-931C-25 Sequence 25, Appl
14	332.5	72.4	90	4	US-09-516-052-31 Sequence 31, Appl
15	332.5	72.4	90	4	US-09-516-052-34 Sequence 34, Appl
16	332.5	72.4	90	4	US-09-516-052-35 Sequence 35, Appl
17	331.5	72.2	90	3	US-09-103-478-22 Sequence 22, Appl
18	331.5	72.2	90	3	US-09-193-931C-22 Sequence 22, Appl
19	331.5	72.2	90	4	US-09-516-052-32 Sequence 32, Appl
20	329.5	71.8	90	3	US-09-103-478-25 Sequence 25, Appl
21	329.5	71.8	90	3	US-09-193-931C-26 Sequence 26, Appl
22	329.5	71.8	90	4	US-09-516-052-36 Sequence 36, Appl
23	323.5	70.5	146	4	US-09-435-05A-8 Sequence 8, Appl
24	323.5	70.5	240	4	US-09-435-05A-10 Sequence 10, Appl
25	323.5	70.5	355	4	US-09-435-05A-18 Sequence 18, Appl
26	322.5	70.3	214	4	US-09-435-05A-12 Sequence 12, Appl
27	319.5	69.6	205	4	US-09-516-052-20 Sequence 20, Appl

ALIGNMENTS

RESULT 1
 US-09-103-478-20
 Sequence 20, Application US/09103478
 Patent No. 6235975
 GENERAL INFORMATION:
 APPLICANT: Harada, John
 APPLICANT: Lotan, Tamar
 APPLICANT: Ohto, Masaki
 APPLICANT: Goldberg, Robert B.
 APPLICANT: Fischer, Robert L.
 TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-9344

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/103,478
 FILING DATE: 24-JUN-1998
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/026,221
 FILING DATE: 13-FEB-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/804,534
 FILING DATE: 21-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Birnboim, Gregory P.
 REGISTRATION NUMBER: 38,440
 REFERENCE DOCKET NUMBER: 023070-077611US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0300
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 90 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-103-478-20
 Sequence 20, Appl

Query Match 87.7%; Score 402.5; DB 3; Length 90; Best Local Similarity 83.5%; Pred. No. 3_9e-52; Mismatches 2; Indels 7; Gaps 1; Matches 81; Conservative

Qy 1 RSDQRFLPIANISRIMKKALPKNGKXXXXXXTAKDAKXTKBCVSERISFTSEASXKC 60
Db 1 RSDQRFLPIANISRIMKKALPKNGKXXXXXXTAKDAKXTKBCVSERISFTSEASXKC 53

Qy 61 QSERKRTINGDDLLWAMATLGFDYIPLKVLYKXR 97
Db 54 QSERKRTINGDDLLWAMATLGFDYIPLKVLYKXR 90

RESULT 2
US-09-193-931C-20
; Sequence 20, Application US/09193931C
; Patent No. 6320102
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; APPLICANT: The Regents of the University of California
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
FILE REFERENCE: 024070-077620
CURRENT APPLICATION NUMBER: US/09/193,931C
CURRENT FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 09/103,478
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 09/026,221
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: US 08/804,534
PRIOR FILING DATE: 1997-02-21
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 90
TYPE: PRT
ORGANISM: Zea mays
FEATURE: DOMAIN
NAME/KS: DOMAIN
LOCATION: (1)..(90)
OTHER INFORMATION: maize HAP3 subunit of CCAAT box-binding factor
OTHER INFORMATION: (CBP) protein B domain homolog

US-09-516-052-30
Query Match 87.7%; Score 402.5; DB 4; Length 90; Best Local Similarity 83.5%; Pred. No. 3_9e-52; Mismatches 2; Indels 7; Gaps 1; Matches 81; Conservative

Qy 1 RSDQRFLPIANISRIMKKALPKNGKXXXXXXTAKDAKXTKBCVSERISFTSEASXKC 60
Db 1 RSDQRFLPIANISRIMKKALPKNGKXXXXXXTAKDAKXTKBCVSERISFTSEASXKC 53

Qy 61 QSERKRTINGDDLLWAMATLGFDYIPLKVLYKXR 97
Db 54 QSERKRTINGDDLLWAMATLGFDYIPLKVLYKXR 90

RESULT 3
US-09-516-052-30
; Sequence 30, Application US/09516052
; Patent No. 6781035
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-Aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; APPLICANT: Bui, Anhthu
; APPLICANT: Khong, Raymond
; APPLICANT: The Regents of the University of California

Query Match 87.7%; Score 401.5; DB 4; Length 218; Best Local Similarity 78.2%; Pred. No. 1_7e-51; Mismatches 5; Indels 7; Gaps 1; Matches 79; Conservative

Qy 1 RSDQRFLPIANISRIMKKALPKNGKXXXXXXTAKDAKXTKBCVSERISFTSEASXKC 60
Db 34 RSDQRFLPIANISRIMKKALPKNSAK-----ISDAKXTKBCVSERISFTSEASXKC 86

Qy 61 QSERKRTINGDDLLWAMATLGFDYIPLKVLYKXR 101
Db 87 QSERKRTINGDDLLWAMATLGFDYIPLKVLYKXRLEG 127

RESULT 5
US-09-640-211A-1051
; Sequence 1051; Application US/09640211A
; GENERAL INFORMATION:
; APPLICANT: Wood, Marlon
; APPLICANT: Shank, Michael A.
; APPLICANT: McCrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000-1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 1051
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Pinus radiata
; US-09-640-211A-1051

Query Match
Best Local Similarity 86.6%; Score 397.5; DB 4; Length 219;
Matches 76; Conservative 7; Mismatches 11; Indels 7; Gaps 1;

Qy 1 REQDRYLPANIRIMKALPKXNGXXXXXAKDAKTXQCVSERTISFTSEASKC 60
Db 24 KEDQRFLPLIANVGRIMKGALPANGK-----VSQDAETVQBCVSERTISFTGEASDKC 76

Qy 61 QXERKRKTINGDDLIWAMATLGFDYIPLKVLYKXREKG 101
Db 77 QRSKRKTINGDDLIWAMTTLGFDYIPLKVLYKXREKG 117

RESULT 6
US-09-538-092-1008
; Sequence 1008; Application US/09538092
; PATENT INFORMATION:
; APPLICANT: Gior, Lotc
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 1536-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 6/01277,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 6/01787,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: ClustalSeqFormatter Version 0.9
; SEQ ID NO: 1008
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P25208

Query Match
Best Local Similarity 67.3%; Score 337.5; DB 4; Length 207;
Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REBDRYLPLANIRIMKALPKXNGXXXXXAKDAKTXQCVSERTISFTSEASKC 60
Db 53 REGDYLPLIANVGRIMKGALPANGK-----IAKDAETVQBCVSERTISFTSEASKC 105

Query Match
Best Local Similarity 75.2%; Score 397.5; DB 4; Length 219;
Matches 76; Conservative 7; Mismatches 11; Indels 7; Gaps 1;

Qy 1 REQDRYLPANIRIMKALPKXNGXXXXXAKDAKTXQCVSERTISFTSEASKC 60
Db 24 KEDQRFLPLIANVGRIMKGALPANGK-----VSQDAETVQBCVSERTISFTGEASDKC 76

Qy 61 QXERKRKTINGDDLIWAMATLGFDYIPLKVLYKXREKG 101
Db 77 QRSKRKTINGDDLIWAMTTLGFDYIPLKVLYKXREKG 117

RESULT 7
US-09-949-016-7348
; Sequence 7348; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.
; TITLE OF INVENTION: Polymorphisms in Known Genes Associated
; TITLE OF INVENTION: With Human Disease, Methods of Detection and Uses Thereof
; FILE REFERENCE: CLO001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 601241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 601237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 7348
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7348

Query Match
Best Local Similarity 67.3%; Score 337.5; DB 4; Length 211;
Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REQDRYLPANIRIMKALPKXNGXXXXXAKDAKTXQCVSERTISFTSEASKC 60
Db 56 REQDRYLPANVARIMKGALPQGK-----IAKDAETVQBCVSERTISFTSEASKC 108

Qy 61 QXERKRKTINGDDLIWAMATLGFDYIPLKVLYKXREKG 98
Db 109 HQSKRKTINGDDLIWAMSTLGFDSYVEPLKVLYQKFRE 146

RESULT 8
US-09-103-478-21
; Sequence 21; Application US/09103478
; Patent No. 6233975
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Otoh, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: LRFY COTyledoni Genes and Their Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,478
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,221
; FILING DATE: 19-FEB-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/804, 534
 FILING DATE: 21-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Eihorn, Gregory P.
 REGISTRATION NUMBER: 38,440
 REFERENCE/DOCKET NUMBER: 023070-077611US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 FAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 90 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-09-103-478-21

Query Match 72.4%; Score 332.5; DB 3; Length 90;
 Best Local Similarity 67.0%; Pred. No. 1.1e-41;
 Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

QV 1 RSDQYDPLIANISRMKQCALPKNGXXXXXXIAKDAKXTKOBCVSFRISFTSEASXC 60
 1 RSDQYDPLIANISRMKQCALPKNGXXXXXXIAKDAKXTKOBCVSFRISFTSEASXC 53

QY 61 QKERRQKTINGDDILWAMATLGFDYIPLKLYLXXYR 97
 54 HOERKRKTINGDDILWAMATLGFDYIPLKLYLXXYR 90

Db 54 HOERKRKTINGDDILWAMATLGFDYIPLKLYLXXYR 90

RESULT 9
 US-09-103-478-24
 Sequence 24, Application US/09103478
 Patent No. 6233975

GENERAL INFORMATION:
 APPLICANT: Harada, John
 APPLICANT: Lotan, Tamar
 APPLICANT: Ohto, Mata-aki
 APPLICANT: Goldberg, Robert B.
 APPLICANT: Fischer, Robert L.

TITLE OF INVENTION: LEAFY COTyledoni Genes and Their Uses
 NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/103, 478
 FILING DATE: 24-JUN-1998
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/026, 221
 FILING DATE: 19-FEB-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/804, 534
 FILING DATE: 21-FEB-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/026, 221
 FILING DATE: 19-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Eihorn, Gregory P.
 REGISTRATION NUMBER: 38,440
 REFERENCE/DOCKET NUMBER: 023070-077611US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 FAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 90 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-09-103-478-24

Query Match 72.4%; Score 332.5; DB 3; Length 90;

INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 90 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-09-103-478-25

Query Match 72.4%; Score 332.5; DB 3; Length 90;
 Best Local Similarity 67.0%; Pred. No. 1.1e-41;
 Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

QV 1 RSDQYDPLIANISRMKQCALPKNGXXXXXXIAKDAKXTKOBCVSFRISFTSEASXC 60
 1 RSDQYDPLIANISRMKQCALPKNGXXXXXXIAKDAKXTKOBCVSFRISFTSEASXC 53

QY 61 QKERRQKTINGDDILWAMATLGFDYIPLKLYLXXYR 97
 54 HOERKRKTINGDDILWAMATLGFDYIPLKLYLXXYR 90

Db 54 HOERKRKTINGDDILWAMATLGFDYIPLKLYLXXYR 90

RESULT 10
 US-09-103-478-25
 Sequence 25, Application US/09103478
 Patent No. 6233975

GENERAL INFORMATION:
 APPLICANT: Harada, John
 APPLICANT: Lotan, Tamar
 APPLICANT: Ohto, Mata-aki
 APPLICANT: Goldberg, Robert B.
 APPLICANT: Fischer, Robert L.

TITLE OF INVENTION: LEAFY COTyledoni Genes and Their Uses
 NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/103, 478
 FILING DATE: 24-JUN-1998
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/026, 221
 FILING DATE: 19-FEB-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/804, 534
 FILING DATE: 21-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Eihorn, Gregory P.
 REGISTRATION NUMBER: 38,440
 REFERENCE/DOCKET NUMBER: 023070-077611US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 FAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 90 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-09-103-478-25

Query Match 72.4%; Score 332.5; DB 3; Length 90;

Best Local Similarity 67.0%; Pred. No. 1.1e-41; Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1; Current Filing Date: 1998-11-17; Prior Application Number: US 09/103,473

Query Match 1 REQDYLPLANTSRIMKALPKNGXXXXXXIAKDAKTXQCVSERISPTSEASRKC 60
 Database 1 REQDYLPLANTSRIMKALPKNGXXXXXXIAKDAKTXQCVSERISPTSEASRKC 53
 Prior Application Number: US 09/036,221
 Prior Filing Date: 1998-06-24
 Prior Filing Date: 1997-02-21
 Number of Seq ID Nos: 29
 Software: PatentIn Ver. 2.0
 Seq ID No: 24
 Length: 90
 Type: PRT
 Organism: Homo sapiens
 Feature:
 Name/Key: DOMAIN
 Location: (1)..(90)
 Other Information: human HAP3 subunit of CCAAT Box-binding factor
 Other Information: (CBF) protein B domain homolog

US-09-193-931C-21
 Sequence 21, Application US/09193931C
 Patent No. 6320102
 General Information:
 Applicant: Harada, John
 Applicant: Lotan, Tamar
 Applicant: Ohto, Masa-aki
 Applicant: Goldberg, Robert B.
 Applicant: Fischer, Robert L.
 Applicant: The Regents of the University of California
 Title of Invention: LEAFY CORYLEDON1 Genes and Their Uses
 File Reference: 023070-077620
 Current Application Number: US/09/193,931C
 Current Filing Date: 1998-11-17
 Prior Application Number: US 09/103,478
 Prior Filing Date: 1998-06-24
 Prior Application Number: US 09/036,221
 Prior Filing Date: 1997-02-21
 Prior Application Number: US 09/026,221
 Prior Filing Date: 1998-02-19
 Prior Application Number: US 08/804,534
 Prior Filing Date: 1997-02-21
 Number of Seq ID Nos: 29
 Software: PatentIn Ver. 2.0
 Seq ID No: 21
 Length: 90
 Type: PRT
 Organism: Gallus sp.
 Feature:
 Name/Key: DOMAIN
 Location: (1)..(90)
 Other Information: chicken HAP3 subunit of CCAAT box-binding factor
 Other Information: (CBF) protein B domain homolog

US-09-193-931C-21
 Sequence 21, Application US/09193931C
 Patent No. 6320102
 General Information:
 Applicant: Harada, John
 Applicant: Lotan, Tamar
 Applicant: Ohto, Masa-aki
 Applicant: Goldberg, Robert B.
 Applicant: Fischer, Robert L.
 Applicant: The Regents of the University of California
 Title of Invention: LEAFY CORYLEDON1 Genes and Their Uses
 File Reference: 023070-077620
 Current Application Number: US/09/193,931C
 Current Filing Date: 1998-11-17
 Prior Application Number: US 09/103,478
 Prior Filing Date: 1998-06-24
 Prior Application Number: US 09/026,221
 Prior Filing Date: 1998-02-19
 Prior Application Number: US 08/804,534
 Prior Filing Date: 1997-02-21
 Prior Application Number: US 09/026,221
 Prior Filing Date: 1998-02-19
 Prior Application Number: US 08/804,534
 Prior Filing Date: 1997-02-21
 Number of Seq ID Nos: 29
 Software: PatentIn Ver. 2.0
 Seq ID No: 21
 Length: 90
 Type: PRT
 Organism: Mus musculus and Rattus norvegicus
 Feature:
 Name/Key: DOMAIN
 Location: (1)..(90)
 Other Information: mouse/rat HAP3 subunit of CCAAT box-binding factor
 Other Information: (CBF) protein B domain homolog

RESULT 12
 US-09-193-931C-24
 Sequence 24, Application US/09193931C
 Patent No. 6320102
 General Information:
 Applicant: Harada, John
 Applicant: Lotan, Tamar
 Applicant: Ohto, Masa-aki
 Applicant: Goldberg, Robert B.
 Applicant: Fischer, Robert L.
 Applicant: The Regents of the University of California
 Title of Invention: LEAFY CORYLEDON1 Genes and Their Uses
 File Reference: 023070-077620
 Current Application Number: US/09/193,931C
 Current Filing Date: 1998-11-17
 Prior Application Number: US 09/103,478
 Prior Filing Date: 1998-06-24
 Prior Application Number: US 09/026,221
 Prior Filing Date: 1998-02-19
 Prior Application Number: US 08/804,534
 Prior Filing Date: 1997-02-21
 Prior Application Number: US 09/026,221
 Prior Filing Date: 1998-02-19
 Prior Application Number: US 08/804,534
 Prior Filing Date: 1997-02-21
 Number of Seq ID Nos: 29
 Software: PatentIn Ver. 2.0
 Seq ID No: 25
 Length: 90
 Type: PRT
 Organism: Mus musculus and Rattus norvegicus
 Feature:
 Name/Key: DOMAIN
 Location: (1)..(90)
 Other Information: mouse/rat HAP3 subunit of CCAAT box-binding factor
 Other Information: (CBF) protein B domain homolog

Query Match 1 REQDYLPLANTSRIMKALPKNGXXXXXXIAKDAKTXQCVSERISPTSEASRKC 60
 Best Local Similarity 67.0%; Pred. No. 1.1e-41; length 90;
 Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

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RESULT 14
US-09-516-052-31
; Sequence 31, Application US/09516052
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-Aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; APPLICANT: Bui, Anhthu
; APPLICANT: Khong, Raymond
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: LEAFY CORYLDON Genes and Their Use
; FILE REFERENCE: 023070-077630US
; CURRENT APPLICATION NUMBER: US/09/516,052
; PRIORITY APPLICATION NUMBER: US 09/193,931
; PRIORITY FILING DATE: 1998-11-17
; PRIORITY APPLICATION NUMBER: US 09/103,478
; PRIORITY FILING DATE: 1997-02-21
; PRIORITY APPLICATION NUMBER: US 09/026,221
; PRIORITY FILING DATE: 1998-02-19
; PRIORITY APPLICATION NUMBER: US 08/804,534
; PRIORITY FILING DATE: 1997-02-21
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(90)
; OTHER INFORMATION: human HAP3 subunit of CCAAT Box-binding factor
; OTHER INFORMATION: (CBF) protein B domain homolog
US-09-516-052-34
Query Match
Best Local Similarity 72.4%; Score 332.5; DB 4; Length 90;
Matches 65; Conservative 67.0%; Pred. No. 1.1e-41; Mismatches 13; Indels 7; Gaps 1;
Query 1 RQDYLPTANRIMKPKALPANGICXXXXXXTAKDAKTKXQECVSERPSFTSEASRC 60
Db 1 RQDYLPTANRIMKPKALPANGICXXXXXXTAKDAKTKXQECVSERPSFTSEASRC 53
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Db 54 HQERKRTINGDDLWAMATIGFEDIEPKVLYKXR 90

RESULT 15
US-09-516-052-34
; Sequence 34, Application US/09516052
; GENERAL INFORMATION:
; PATENT NO. 6781035
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-Aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; APPLICANT: Bui, Anhthu
; APPLICANT: Khong, Raymond
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: LEAFY CORYLDON Genes and Their Use
; FILE REFERENCE: 023070-077630US

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OM protein - protein search, using SW model
Run on: November 17, 2005, 08:52:50 ; Search time 165 seconds
(without alignments)
256.117 Million cell updates/sec

Title: US-10-678-588a-8
Perfect score: 459
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA,*

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21: /cgmn_6/ptodata/1/pubpa/US11B_PUBCOMB.pep:*

22: /cgmn_6/ptodata/1/pubpa/US60_PUBCOMB.pep:*

RESULT 1
US-10-678-588a-8
Publication No. US2005002266A1
GENERAL INFORMATION:
APPLICANT: Wu, Jingrui
TITLE OF INVENTION: Water-Deficit-Tolerant Transgenic Plants
FILE REFERENCE: 38-21 (S2578C
CURRENT APPLICATION NUMBER: US/10/678,588A
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,758
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US 60/425,157
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 60/463,787
NUMBER OF SEQ ID NOS: 10
SEQUENCE: PatentIn version 3.2
SEQ ID NO: 8
LENGTH: 101
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE: OTHER INFORMATION: protein consensus sequence
FEATURE: OTHER INFORMATION: protein consensus sequence
NAME/KEY: MISC FEATURE
LOCATION: (22)-(22)
OTHER INFORMATION: Xaa can be Ala or Pro
FEATURE: OTHER INFORMATION: Xaa can be Ala or Pro
NAME/KEY: MISC FEATURE
LOCATION: (26)-(26)
OTHER INFORMATION: Xaa can be Thr or none
FEATURE: NAME/KEY: MISC FEATURE

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	# Query	Match Length	DB ID	Description
1	429	93.5	101	17	US-10-678-588a-8 Sequence 8, Appl1
2	425	92.6	185	17	US-10-678-588a-2 Sequence 2, Appl1
3	425	92.6	185	17	US-10-675-852-42 Sequence 42, Appl1
4	423.5	92.3	160	15	US-10-774-700-802 Sequence 802, Appl1
5	423.5	92.3	160	17	US-10-675-852-26 Sequence 26, Appl1
6	423.5	92.3	173	15	US-10-424-559-27836 Sequence 274836, Appl1
7	423.5	92.3	173	17	US-10-678-588a-6 Sequence 6, Appl1
8	423.5	92.3	173	17	US-10-675-852-24 Sequence 24, Appl1
9	423.5	92.3	174	15	US-10-24-559-27840 Sequence 274840, Appl1
10	423.5	92.3	174	15	US-10-425-114-39733 Sequence 39733, Appl1
11	423.5	92.3	174	17	US-10-675-852-84 Sequence 84, Appl1

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; LOCATION: (27)...(27)
; OTHER INFORMATION: Xaa can be Ile or none
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (28)...(28)
; OTHER INFORMATION: Xaa can be Pro or none
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (29)...(29)
; OTHER INFORMATION: Xaa can be Ala or none
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (30)...(30)
; OTHER INFORMATION: Xaa can be Asn or none
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (31)...(31)
; OTHER INFORMATION: Xaa can be Gly or none
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (32)...(32)
; OTHER INFORMATION: Xaa can be Lys or none
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (39)...(39)
; OTHER INFORMATION: Xaa can be Glu or Asp
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (41)...(41)
; OTHER INFORMATION: Xaa can be Val or Met
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (58)...(58)
; OTHER INFORMATION: Xaa can be Asp or Glu
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (62)...(62)
; OTHER INFORMATION: Xaa can be Arg or Lys
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (94)...(94)
; OTHER INFORMATION: Xaa can be Gln or Ala
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (95)...(95)
; OTHER INFORMATION: Xaa can be Lys or Arg
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (99)...(99)
; OTHER INFORMATION: Xaa can be Met or Ala
; US-10-678-588A-8

Query Match 92.6%; Score 425; DB 17; length 185;
Best Local Similarity 83.2%; Pred. No. 4 7e-10; 2; Mismatches 15; Indels 0; Gaps 0;
Matches 84; Conservative 84; Publication No. US20050086718A1
Ov 1 RSDRDRYPIANTSRIMKALPKNGKXXXXXIAKDAKXTKORCVSFRISFTSEASKC 60
Db 30 REBDRFLPIANISRIMKKAIPANGKIAKDKTVOECVSFRISFTSEASDC 89
Qv 61 QEKRKRTINGDILWAMATLGFDYIPLKVYLQKYREMEG 101
Dd 90 QREKRKRTINGDILWAMATLGFDYIPLKVYLQKYREMEG 130

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RESULT 3
US-10-675-852-42
Sequence 42, Application US/10675852
Publication No. US20050086718A1
GENERAL INFORMATION:
APPLICANT: Mandel Biotechnology, Inc.
APPLICANT: HEARD, Jacqueline E.
APPLICANT: KEDDIE, James S.
APPLICANT: CREELMAN, Robert A.
APPLICANT: PINEDA, Omaira
APPLICANT: JIANG, Cai-Zhong
APPLICANT: RATCLIFFE, Oliver
APPLICANT: KUMIMO, Roderick
APPLICANT: GUTTERSON, Neal
APPLICANT: SHERMAN, Bradley K.
TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS
FILE REFERENCE: MB1-002CIP
CURRENT APPLICATION NUMBER: US/10/675,852
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: 10/412,699
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/713,994
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 60/166,228
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/197,899
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 60/227,439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 10/112,887
PRIOR FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 10/286,264
PRIOR FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
TYPE: PRT
ORGANISM: Zea mays
US-10-678-588A-2
LENGTH: 185

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RESULT 2  
US-10-678-588A-2  
Sequence 2, Application US/10678588A  
Publication No. US2005002266A1  
GENERAL INFORMATION:  
APPLICANT: WU, Jingrui  
TITLE OF INVENTION: Water-Deficit-Tolerant Transgenic Plants  
FILE REFERENCE: 38-21(52578)C  
LENGTH: 185

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US-10-374-780A-802

Query Match 92.3%; Score 423.5; DB 15; Length 160;
Best Local Similarity 85.1%; Pred. No. 6; 3e-50; Indels 7; Gaps 1;
Organism: Zea mays
Feature: OTHER INFORMATION: ZEAMA-0BNOV01-CLUSTER719_3 polypeptide
US-10-675-852-42

Query Match 92.3%; Score 423.5; DB 15; Length 160;
Best Local Similarity 85.1%; Pred. No. 6; 3e-50; Indels 7; Gaps 1;
Organism: Zea mays
Feature: OTHER INFORMATION: ZEAMA-0BNOV01-CLUSTER719_3 polypeptide
US-10-675-852-42

RESULT 4

US-10-374-780A-802

; Sequence 802, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S
; APPLICANT: Brown, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MB1-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIORITY APPLICATION NUMBER: 09/1837,944
PRIORITY FILING DATE: 2001-04-18
PRIORITY APPLICATION NUMBER: 60/310,847
PRIORITY FILING DATE: 2001-08-09
PRIORITY APPLICATION NUMBER: 09/934,455
PRIORITY FILING DATE: 2001-08-22
PRIORITY APPLICATION NUMBER: 60/336,049
PRIORITY FILING DATE: 2001-11-19
PRIORITY APPLICATION NUMBER: 60/338,692
PRIORITY FILING DATE: 2001-12-11
PRIORITY APPLICATION NUMBER: 10/171,468
PRIORITY FILING DATE: 2002-06-14
PRIORITY APPLICATION NUMBER: 10/125,066
PRIORITY FILING DATE: 2002-08-09
PRIORITY APPLICATION NUMBER: 10/225,067
PRIORITY FILING DATE: 2002-08-09
PRIORITY APPLICATION NUMBER: 10/225,068
PRIORITY FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 802
LENGTH: 160
TYPE: PRT
ORGANISM: Glycine max
FEATURE: OTHER INFORMATION: Orthologous to G481, G482
FEATURE: NAME/KEY: misc feature
LOCATION: (151)..(151)
LOCATION: (151)..(151)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid

RESULT 5

US-10-675-852-26

; Sequence 26, Application US/10675852
; Publication No. US20050086718A1
; GENERAL INFORMATION:
; APPLICANT: Mendl, Biotechnology, Inc.
; APPLICANT: Heard, Jacqueline E
; APPLICANT: KEDDIE, James S
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: KOMIMOTO, Roderick
; APPLICANT: GUTTERSON, Neal
; APPLICANT: SHERMAN, Bradley K
TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS
FILE REFERENCE: MB1-0022CIP
CURRENT APPLICATION NUMBER: US/10/675,852
CURRENT FILING DATE: 2003-09-30
PRIORITY APPLICATION NUMBER: 10/412,699
PRIORITY FILING DATE: 2003-04-10
PRIORITY APPLICATION NUMBER: 09/533,030
PRIORITY FILING DATE: 2000-03-22
PRIORITY APPLICATION NUMBER: 60/125,814
PRIORITY FILING DATE: 1999-03-23
PRIORITY APPLICATION NUMBER: 09/713,994
PRIORITY FILING DATE: 2000-11-16
PRIORITY APPLICATION NUMBER: 09/166,228
PRIORITY FILING DATE: 1999-11-17
PRIORITY APPLICATION NUMBER: 60/197,899
PRIORITY FILING DATE: 2000-04-17
PRIORITY APPLICATION NUMBER: 60/227,439
PRIORITY FILING DATE: 2000-08-22
PRIORITY APPLICATION NUMBER: 10/112,887
PRIORITY FILING DATE: 2003-03-18
PRIORITY APPLICATION NUMBER: 10/286,264
PRIORITY FILING DATE: 2003-01-23
PRIORITY APPLICATION NUMBER: 10/225,058
PRIORITY FILING DATE: 2002-08-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 26
LENGTH: 160
TYPE: PRT
ORGANISM: Glycine max
FEATURE: OTHER INFORMATION: Glycine max
FEATURE: NAME/KEY: misc feature
LOCATION: (151)..(151)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE: OTHER INFORMATION: G3470 GLYMA-28NOV01-CLUSTER4778_3 polypeptide
US-10-675-852-26

Query Match 92.3%; Score 423.5; DB 15; Length 160;
Best Local Similarity 85.1%; Pred. No. 6; 3e-50; Indels 7; Gaps 1;
Organism: Zea mays
Feature: OTHER INFORMATION: G3470 GLYMA-28NOV01-CLUSTER4778_3 polypeptide
US-10-675-852-42

RESULT 6

US-10-374-780A-802

; Sequence 802, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S
; APPLICANT: Brown, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MB1-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIORITY APPLICATION NUMBER: 09/1837,944
PRIORITY FILING DATE: 2001-04-18
PRIORITY APPLICATION NUMBER: 60/310,847
PRIORITY FILING DATE: 2001-08-09
PRIORITY APPLICATION NUMBER: 09/934,455
PRIORITY FILING DATE: 2001-08-22
PRIORITY APPLICATION NUMBER: 60/336,049
PRIORITY FILING DATE: 2001-11-19
PRIORITY APPLICATION NUMBER: 60/338,692
PRIORITY FILING DATE: 2001-12-11
PRIORITY APPLICATION NUMBER: 10/171,468
PRIORITY FILING DATE: 2002-06-14
PRIORITY APPLICATION NUMBER: 10/125,066
PRIORITY FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 802
LENGTH: 160
TYPE: PRT
ORGANISM: Glycine max
FEATURE: OTHER INFORMATION: Orthologous to G481, G482
FEATURE: NAME/KEY: misc feature
LOCATION: (151)..(151)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE: OTHER INFORMATION: G3470 GLYMA-28NOV01-CLUSTER4778_3 polypeptide
US-10-675-852-42

RESULT 6
US-10-424-599-274836
 ; Sequence 6, Application US/10424599
 ; Publication No. US2004031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovacic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TUTOR OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 274536
 ; LENGTH: 173
 ; FEATURE:
 ; ORGANISM: Glycine max
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_30198C.1.pep
 US-10-424-599-274836

RESULT 8
US-10-675-852-24
 ; Sequence 24, Application US/10675852
 ; Publication No. US20050086718A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mandel Biotechnology, Inc.
 ; APPLICANT: Head, Jacqueline E
 ; APPLICANT: Keddie, James S
 ; APPLICANT: Creelman, Robert A
 ; APPLICANT: Pineda, Omaha
 ; APPLICANT: Jiang, Cai-Zhong
 ; APPLICANT: Ratcliffe, Oliver
 ; APPLICANT: Kumimoto, Roderick
 ; APPLICANT: Gutierrez, Neal
 ; APPLICANT: Sherman, Bradley K
 ; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS
 ; FILE REFERENCE: MDI-0022CIP
 ; CURRENT APPLICATION NUMBER: US/10/675,852
 ; CURRENT FILING DATE: 2003-09-30
 ; PRIORITY FILING DATE: 2003-04-10
 ; PRIORITY APPLICATION NUMBER: 10/412,699
 ; PRIORITY APPLICATION NUMBER: 09/533,030
 ; PRIORITY FILING DATE: 2000-03-22
 ; PRIORITY APPLICATION NUMBER: 60/125,814
 ; PRIORITY FILING DATE: 1998-03-23
 ; PRIORITY APPLICATION NUMBER: 09/713,994
 ; PRIORITY FILING DATE: 2000-11-16
 ; PRIORITY APPLICATION NUMBER: 60/166,228
 ; PRIORITY FILING DATE: 1998-11-17
 ; PRIORITY APPLICATION NUMBER: 60/197,899
 ; PRIORITY FILING DATE: 2000-04-17
 ; PRIORITY APPLICATION NUMBER: 60/227,439
 ; PRIORITY FILING DATE: 2000-08-22
 ; PRIORITY APPLICATION NUMBER: 10/112,887
 ; PRIORITY FILING DATE: 2003-03-18
 ; PRIORITY APPLICATION NUMBER: 10/286,264
 ; PRIORITY APPLICATION NUMBER: 10/225,068
 ; PRIORITY FILING DATE: 2003-01-23
 ; PRIORITY APPLICATION NUMBER: 10/099
 ; Remaining Prior Application data removed - See file wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 104
 ; SEQ ID NO 24
 ; LENGTH: 173
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: G3471_GLYMA-28NOV01-CLUSTER4778_1 polypeptide
 US-10-675-852-24

RESULT 7
US-10-678-588a-6
 ; Sequence 6, Application US/10678588A
 ; Publication No. US2005002266A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wu, Jingrui
 ; TITLE OF INVENTION: Water-Deficit-Tolerant Transgenic Plants
 ; FILE REFERENCE: 38-21(5578)C
 ; CURRENT APPLICATION NUMBER: US/10/678,588A
 ; CURRENT FILING DATE: 2003-10-02
 ; PRIOR APPLICATION NUMBER: US 60/415,758
 ; PRIOR FILING DATE: 2002-10-02
 ; PRIOR APPLICATION NUMBER: US 60/425,157
 ; PRIOR FILING DATE: 2002-11-08
 ; PRIOR APPLICATION NUMBER: US 60/463,787
 ; PRIOR FILING DATE: 2003-04-11
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.2
 ; SEO_ID NO 6
 ; LENGTH: 173
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; OTHER INFORMATION: G3471_GLYMA-28NOV01-CLUSTER4778_1 polypeptide
 US-10-678-588a-6

Query Match 92.3%; Score 423.5; DB 17; Length 173;
 Best Local Similarity 85.1%; Pred. No. 6.9e-50; Indels 7; Gaps 1;
 Matches 86; Conservative 0; Mismatches 8;

Query Match 92.3%; Score 423.5; DB 17; Length 173;
 Best Local Similarity 85.1%; Pred. No. 6.9e-50; Indels 7; Gaps 1;
 Matches 86; Conservative 0; Mismatches 8;

RESULT 9

US-10-424-599-274840

; Sequence 274840, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; PLANT IMPROVEMENT

; FILE REFERENCE: 38-21(55223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; SEQ ID NO: 274840

; LENGTH: 174

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_90200C.1.pep

; US-10-424-599-274840

; Query Match Best Local Similarity 92.3%; Score 423.5; DB 15; Length 174;

; Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

; Qy 1 REQDRYLIANTSRIMKCALPANGXXXXXXTAKDAKTXKBCVSFISFTSEASKC 60

; Db 27 REQDRYLIANTSRIMKCALPANGXXXXXXTAKDAKTXKBCVSFISFTSEASKC 79

; Qy 61 QKEKRKTINGDDLIWAMATLGFDYIEPLKVYLXXYREXEG 101

; Db 80 QKEKRKTINGDDLIWAMATLGFDYIEPLKVYLARYRREG 120

; RESULT 10

; US-10-425-114-39733

; Sequence 39733, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E.

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(55313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO: 39733

; LENGTH: 174

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE: OTHER INFORMATION: Clone ID: 700677948_FLI.pep

; US-10-425-114-39733

; Query Match Best Local Similarity 92.3%; Score 423.5; DB 15; Length 174;

; Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_90200C.1.pep

; US-10-425-114-39733

; Query Match Best Local Similarity 92.3%; Score 423.5; DB 15; Length 174;

; Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

; Qy 1 REQDRYLIANTSRIMKCALPANGXXXXXXTAKDAKTXKBCVSFISFTSEASKC 60

; Db 27 REQDRYLIANTSRIMKCALPANGXXXXXXTAKDAKTXKBCVSFISFTSEASKC 79

; Qy 61 QKEKRKTINGDDLIWAMATLGFDYIEPLKVYLXXYREXEG 101

; Db 80 QKEKRKTINGDDLIWAMATLGFDYIEPLKVYLARYRREG 120

; RESULT 11

; US-10-675-852-84

; Sequence 84, Application US/10675852

; Publication No. US20050086718A1

; GENERAL INFORMATION:

; APPLICANT: Mendel Biotechnology, Inc.

; APPLICANT: Heard, Jacqueline E.

; APPLICANT: KEDDIB, James S

; APPLICANT: CREELMAN, Robert A

; APPLICANT: PINEDA, Omaha

; APPLICANT: JIANG, Cai-Zhong

; APPLICANT: RATCLIFFE, Oliver

; APPLICANT: KOMIMOTO, Roderick

; APPLICANT: GITTNERSON, Neal

; APPLICANT: SHERMAN, Bradley K

; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOtic STRESS

; FILE REFERENCE: MB1-0022CIP

; CURRENT APPLICATION NUMBER: US/10/675,852

; CURRENT FILING DATE: 2003-03-30

; PRIOR APPLICATION NUMBER: 10/412,699

; PRIOR FILING DATE: 2003-04-10

; PRIOR APPLICATION NUMBER: 09/533,030

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 60/125,814

; PRIOR FILING DATE: 1999-03-23

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; PRIOR FILING DATE: 2002-03-18

; PRIOR APPLICATION NUMBER: 10/286,264

; PRIOR FILING DATE: 2003-01-23

; PRIOR APPLICATION NUMBER: 10/225,068

; PRIOR FILING DATE: 2002-08-09

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 84

; LENGTH: 174

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE: OTHER INFORMATION: G3477 polypeptide

; US-10-675-852-84

; Query Match Best Local Similarity 92.3%; Score 423.5; DB 17; Length 174;

; Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

; Qy 1 REQDRYLIANTSRIMKCALPANGXXXXXXTAKDAKTXKBCVSFISFTSEASKC 60

; Db 27 REQDRYLIANTSRIMKCALPANGXXXXXXTAKDAKTXKBCVSFISFTSEASKC 79

; Qy 61 QKEKRKTINGDDLIWAMATLGFDYIEPLKVYLXXYREXEG 101

; Db 80 QKEKRKTINGDDLIWAMATLGFDYIEPLKVYLARYRREG 120

; RESULT 12

; US-10-425-114-48992

; Sequence 48992, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Tabaska, Jack E.

; APPLICANT: Cao, Yongwei

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E.

APPlicant: Cao, Yongwei
 Title of Invention: Nucleic Acid Molecules and Other Molecules Associated With
 Title of Invention: Plants and Uses Thereof for Plant Improvement
 File Reference: 38-21(5323)B
 Current Application Number: US/10/425, 114
 Number of SEQ ID Nos: 73128
 SEQ ID NO 48992
 Length: 185
 Type: PRT
 Organism: Glycine max
 Feature:
 OTHER INFORMATION: Clone ID: 700554268_FLI.pep
 US-10-425-114-48992

Query Match 92.3%; Score 423.5; DB 15; Length 185;
 Best Local Similarity 85.1%; Pred. No. 5e-50; Mismatches 8; Indels 7; Gaps 1;
 Matches 86; Conservative 0; Prior Application Number: 09/713, 994

QY 1 R E Q D R Y L P I A N I S R I M K A L P X G K X X X X X I A K D A K T X Q O C V S E R I S F T S E A S K C 60
 DB 38 R E Q D R Y L P I A N I S R I M K A L P X G K - - - - - I A K D A K T M Q C V S E R I S F T S E A S K C 90

QY 61 Q X E R K T I N G D D L I W A M A T I G F S D Y I E P L K V Y L X Y R X E G 101
 DB 91 Q X E R K T I N G D D L I W A M A T I G F S D Y I E P L K V Y L X Y R X E G 131

RESULT 13
 US-10-739-930-9314
 Sequence 9314, Application US/10739930
 Publication No. US20040216190A1

GENERAL INFORMATION:

Applicant: Kovacic, David K.
 Title of Invention: NUCLEAR ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH FILE REFERENCE: 38-21(5337)B
 CURRENT APPLICATION NUMBER: US/10/739, 930
 TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
 NUMBER OF SEQ ID NOS: 11088
 SEQ ID NO 9314
 LENGTH: 171
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: GLYMA-23APR03-C6781_1.p
 US-10-739-930-9314

Query Match 91.6%; Score 420.5; DB 16; Length 171;
 Best Local Similarity 83.2%; Pred. No. 1.8e-49; Mismatches 8; Indels 7; Gaps 1;
 Matches 84; Conservative 2; Prior Application Number: 10/225, 068

SEQ ID NO 9314

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 104
 SEQ ID NO 64
 LENGTH: 176
 Type: PRT
 Organism: Lycopersicon esculentum
 Feature:
 OTHER INFORMATION: SGN-UNIGENE-46859 polypeptide

US-10-675-882-64

Query Match 91.6%; Score 420.5; DB 17; Length 176;
 Best Local Similarity 84.2%; Pred. No. 1.8e-49; Mismatches 8; Indels 7; Gaps 1;
 Matches 85; Conservative 1; Prior Application Number: 10/225, 068

QY 1 R E Q D R Y L P I A N I S R I M K A L P X G K X X X X X I A K D A K T X Q O C V S E R I S F T S E A S K C 60
 DB 33 R E Q D R Y L P I A N I S R I M K A L P X G K - - - - - I A K D A K T V Q O C V S E R I S F T S E A S K C 85

QY 61 Q X E R K T I N G D D L I W A M A T I G F S D Y I E P L K V Y L X Y R X E G 101
 DB 86 Q X E R K T I N G D D L I W A M A T I G F S D Y I E P L K V Y L X Y R X E G 126

RESULT 14
 US-10-675-882-64
 Sequence 64, Application US/10675852
 Publication No. US20050086718A1

GENERAL INFORMATION:

Applicant: Mendel Biotechnology, Inc.
 Applicant: Heard, Jacqueline B
 Applicant: Keeble, James S
 Applicant: Cressman, Robert A
 Applicant: Pineda, Omaira
 Applicant: Jiang, Cai-Zhong
 Applicant: Ratcliffe, Oliver

RESULT 15
 US-10-24-599-195353
 Sequence 195353, Application US/10424599
 Publication No. US20040031072A1

GENERAL INFORMATION:

Applicant: La Rosa, Thomas J
 Applicant: Kovacic, David K
 Applicant: Zhou Yihua
 Applicant: Cao Yongwei
 Title of Invention: Soy Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants and Uses Thereof for Plant Improvement
 File Reference: 38-21(5223)B
 Current Application Number: US/10/424, 539
 Number of SEQ ID NOS: 285684
 SEQ ID NO 195353
 Length: 171
 Type: PRT
 Organism: Glycine max
 Feature:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_18430C_1.pep
 US-10-424-599-195353

Search completed: November 17, 2005, 09:02:28
Job time : 166 secs

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